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GenCore version 5.1.6
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December 29, 2005, 22:08:41; Search time 6729 Seconds (without alignments) 12786.661 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-696-686-47 1839 Title: Perfect score:

Scoring table:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

82156650 Total number of hits satisfying chosen parameters:

41078325 segs, 23393541228 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

gb_gssl:* gb_gss2:* gb_est1:;
gb_est2:;;
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gb_est6::;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss3:*

ALIGNMENTS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) AK049358
Mus musculus ES cells cDNA, RIKBN full-length enriched library, clone:C330027B02 product:1600025D17RK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENB), full insert Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Math. Enzymol. 303, 19-44 (1999) 10340636 AKO49358.1 GI:26340087
AKO49358.1 GI:26340087
AKEYMORDS W.HTC'S CAP trapper.
SOURCE Mis musculus (house mouse)
ORGANISM Mis musculus ведиелсе RESULT 1 AK049358 LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE ACCESSION PUBMED REFERENCE AUTHORS AUTHORS JOURNAL TITLE

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Inshi,Y., Nakamura,S., Hazama,M., Nishiha,T., Harada,A., Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Oneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000) JOURNAL

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TITLE

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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0; Mismatches
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/strain="C57BL/6J"
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries EST: * Database :

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gb_est1:: gb_est2::; gb_htc:::: gb_est4::; gb_est5::; gb_est7::; gb_gss1::; gb_gss2::; gb_gss2::;

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| Description | AK049358 Mus muscu AK086940 Mus muscu AK085617 Mus muscu AK0131742 Mus muscu AK082340 Mus muscu AK082340 Mus muscu AK082749 Mus muscu AK010702 Mus muscu CR310728 AGENCOURT BL972275 AGENCOURT BU52275 AGENCOURT CR53710 AGENCOURT BU52275 AGENCOURT BU523708 AGENCOURT BU52275 AGENCOURT BU52276 AGENCOURT BU70894 602794679 BI078951 602873203 CK584966 AGENCOURT CK208584 MNS1585 | |
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| SUMMARIES | AK049358 AK086940 AK086940 AK081742 AK031742 AK082340 BC922055 CE53310 CE53310 BC953310 CR553410 CR55456 | |
| * Query Match Length DB | 1117872 1117872 1116884 116886 | |
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| & Query Match | 00000000000000000000000000000000000 | |
| Score | 1799.2 1780 1780 1683 1528 1388.4 1388.4 1345.6 761.2 761.2 771.3 735.6 733.6 734.6 734.6 734.6 735.6 | |
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| CR625170 full-leng CR603815 full-leng | 44 | CR606170 full-leng | • | CRS93913 full-leng | | CR614568 full-leng | CD353185 UI-M-GL0- | BX375141 BX375141 | AY403772 Mus muscu | | BY710119 BY710119 | _ | BX383415 BX383415 | BM545167 AGENCOURT | CR608091 full-leng | CF732471 UI-M-HA0- | BI110829 602895470 | _ | BU510421 AGENCOURT | DN935262 AGENCOURT | BB498921 BB498921 |
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| 1338 | 1393 | 1461 | 1657 | 1659 | 1667 | 1316 | 969 | 1140 | 721 | 942 | 1024 | 991 | 886 | 1136 | 1694 | 665 | 698 | 779 | 944 | 768 | 645 |
| 37.6 | 37.6 | 37.6 | 37.6 | 37.6 | 37.6 | 37.3 | 37.1 | 36.9 | 36.9 | 36.9 | 36.8 | 36.5 | 36.4 | 36.1 | 35.8 | 35.5 | 35.2 | 34.9 | 34.8 | 34.7 | 34.7 |
| 691.6 | 691.6 | 691.6 | 691.6 | 691.6 | 691.6 | 686.2 | 682 | 678.8 | 678.4 | 677.8 | 677 | 672 | 669.4 | 663.8 | 659.2 | 652 | 646.8 | 641.8 | 640.6 | 638.8 | 638.2 |
| 23 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 3.7 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| RESULT 1 AK049358 LOCUS DEFINITION | AK049358 Mus musculus ES cells cDNA, RIKEN full-length enriched library, |
|---|---|
| | clone:C330027E02 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert |
| ACCESSION | |
| VERSION | AK049358.1 GI:26340087 |
| KEYWORDS | HTC; CAP trapper. |
| ORGANISM | Mus musculus (mouse) |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; |
| | Sciurognathi; Muridae; Murinae; Mus. |
| KEFEKENCE | ; ; ; ; |
| AUTHORS | Carningl, P. and Hayashizaki, Y. |
| TITLE | High-efficiency full-length cloning |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) |
| PUBMED | 10349636 |
| REFERENCE | 2 |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., |
| | Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. |
| TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to |
| | prepare full-length cDNA libraries for rapid discovery of new genes |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) |
| PUBMED | 11042159 |
| REFERENCE | e. |
| AUTHORS | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., |
| | Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., |
| | Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., |
| | Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., |
| | Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., |
| | Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., |
| | Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. |
| TITLE | RIKEN integrated sequence analysis (RISA) system384-format |
| | sequencing pipeline with 384 multicapillary sequencer |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) |
| PUBMED | 11076861 |
| REFERENCE | 4 |
| AUTHORS | The RIKEN Genome Exploration Research Group Phase II Team and the |
| | FANTOM Consortium. |
| TITLE | Functional annotation of a full-length mouse CDNA collection |
| JOURNAL | Nature 409, 685-690 (2001) |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (STREN), Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1832)
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    Exploration Research
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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D. Nature 420, 563-573 (2002)

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22. .852
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakayurchi, S., Itsegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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FUNCTIONAL amnotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
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Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
ibrary, clone: B030013D02 produce: 1600025D17RIK PROTEIN (PUTATIVE
RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK085617

AK085617

Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630047M13 product:1600025D17RK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert sequence.

NA AK085617

AK085617

AK085617

HTC; CAP trapper.

Mus musculus (house mouse)

ISM Mus musculus (house mouse)

Kusaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Muridae; Musinae; Mus.

Sciurognathi; Muridae; Musinae; Mus.
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                                     /note="unnamed protein product; 1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE) (SPTR|Q9DAU1, evidence: FASTY, 100%longth, match=828)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagak,T., Harancto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Hayatsu,Y., Kondo,S., Konno,H., Kawai,J., Kojian,Y., Kondo,S., Konno,H., Kawai,J., Kojian,Y., Kondo,S., Konno,H., Kawai,J., Nomura,K., Numazaki,R., Ohno,M., Ohasto,M., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,C., Sakai,C., Sakai,T., Sasaxi,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Direct Submissional
                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaji, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshika, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Nature 409, 685-690 (2001)
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  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Please visit our web site for further out web site for further URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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| AK031742 Mus musculus 11 days embryo head cDNA, RIKEN full-length enriched library, clone:6230400B22 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert sequence. AK031742. AK031742.1 GI:26327580 HTC; CAP trapper. Mus musculus (house mouse) | Muss musucuta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Musnae; Mus. Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) | Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer | 11076861 4 1076861 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Status 409, 685-690 (2001) | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases I to 1684) Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, J., Anizwa, M., Adachi, T., Bono, H., Carninci, P., Adachi, J., Anizwa, M., Adachi, T., Bono, H., Carninci, P., Adachi, J., Anizwa, M., Adachi, T., Bono, H., Carninci, P., Adachi, J., Anizwa, M., A | Fukuda,N., Fululu,N., Hiramcto,K., Hiracka,T., Hirozane,T., Hayashida,K., Hayatsu,N., Hiramcto,K., Hiracka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kaya,S., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Takeda,Y., Tanaka,T., Tomaru,M., Tokaku,A., Shiraki,T., Tamaku,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y. | Direct Submission Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) RIKEN GENOMIC Sciences Center (GSC), Exploration Research Group, RIKEN GENOMIC Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0046, Japan (8-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) CDNA library was prepared and sequenced in Mouse Genome |
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| RESULT 4 AKO31742 LOCUS DEFINITION ACCESSION VERSION VERSION COURCE | REFERENCE AUTHORS TITLE JOURNAL | REFERENCE AUTHORS TITLE JOURNAL PURNED PERFERENCE | AUTHORS | REFERENCE PUTHORS AUTHORS TITLE JOURNAL REFERENCE | AUTHORS TITLE JOURNAL REFERENCE AUTHORS | | TITLE JOURNAL COMMENT |
| 789 GGAACTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGTGTGCAGAAGGC 848 | 969 GACAGCTGCTCCAGCATCAGGTCTCCTTGGCTGCCCTTTCCTTCC | 1089 GGAGGAGCAGAAGCAGCTCTTTCTACACAGTCCCCCTCACGAGCTCCGGGGTCCACC 1148 | 1209 AAGATGCTCACCAGCGCCCCTTCAGCCAGGAAGACTCCGTGCAGCCAGGCCAGG 1268 | 1356 AGAACTTCCAGGACAAACTCGGGTGTGGGGGGGGGGGGG | CCGGGTGTCCACCCACCCCTGAGGACGCCTCATGCTTCTCCCAGGG CTACCAGAGTAAACACCTTTTGGCTTTCGGTTTGGTTCCTGGGTCCTCATCACCTCCAGG CTACCAGAGTAAACACCTTTTGGCTTTCGGTTTGGTTCCTGGGTCCTCATCAGCCTCCA CTACCAGAGTAAACACCTTTTGGCCTTTCGGTTTGGTTCCTGGGTCCTCATCAGCCTCCA | 1586 GAGTGTCCCCTCATCGATCTTTTTTGCCTTTGTCCCCAGGGGCTGGAAGCCA 1627 1596 GAGTGTCCCCTCATCGATCTTTTTTGCCTTTGTCCCCCAGGGGCTGGAAGGCCA 1627 1628 TCACCATCATTGGAGGCTTAACCTGTGAGTACTAGGAGGTGGTGGGAGGCCCGGGGTT 1687 1656 TCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGGAGCGCCCGGGGTT 1715 1688 GGTTTGGGGTAATCACTCACTGGCTTCTAACACTGCAGCCCCCGGGGTT 1715 1688 GGTTTGGGGTAATCACTCACTGGCTTCTAACACTGCAGCCCCC-TTAATACA 1745 1716 GGTTTGGGGTAATCACTCACTGAGCTTCTAACACTGCAGCCCCCTTTAATACA 1775 | GTTCCTTCTGTTGTGGTGACT-CCCACGCCCCACACACACACATAAATTATTTCGAT GTTCCTTCTGTTGTGGTGACTCCCCACGCCCCCACACACA |

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Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fenome.gsc.riken.jp/.

URL:http://fancom.gsc.riken.jp/.

Location/Qualifiers
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/clone_lib="RIKEN full-length enriched
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/db_xref="FANTOW DB:6230400B22"
/db_xref="taxon:10090"
/clone="6230400B22"
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                                                                          /organism="Mus musculus"
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ICKRLLDYSLHKERTGSNRFAKGNETFETLINLHVKGVKYNDIPYERHNETSABVA
DLKKQCDVLVEEFEEVIEDWYRNHQEEDLTFELCANHVLKGKOTSCIAARWSKKGDIA
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/dev_stige="adult"
               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WIR.:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.jp/) for further
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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/db xref="taxon:10090"
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                                                                                                                                                                                                                                                                    AK005532 HTC 03-AFR-2004 Mus musculus adult female placenta cDNA, RIXEN full-length enriched library, clone:1600025917 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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     CTTCTGTTGTGGGTGACTCCCACGCCCCACACACACCATAAAATTATTTCGATGCTGT 1809
                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1553)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK005532.1 GI:12838152
HTC; CAP trapper.
Mus musculus (house mouse)
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Coh, W., Kagawa, I., Kasukawa, T.,
ndo, S., Konno, H., Kouda, M.,
Numazaki, R., Murata, M.,
Numazaki, R., Ohno, M., Ohsato, N.,
Sakai, C., Sakai, K., Sakazume, N.,
hinagawa, A., Shiraki, T.,
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itsunai,T., Tashiro,H., Itoh,M.,
azama,M., Nishine,T., Harada,A.,
cochi,S., Ikegami,T., Kashiwagi,K.,
Izawa,M., Ohara,E., Watahiki,M.,
Izawa,M., Ohara,E., Watahiki,M.,
Yanaka,T., Matsuura,S., Kawai,J.,
Kira,A. and Hayashizaki,Y.
s (RISA) system--384-format
icapillary sequencer
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CCCCCCTGGAAAGCCAATCTGCAGTTC 1448
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/db_xref="G1:26349663"
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramateu,M. and Hayashizaki,Y.
Muramateu,M. and Hayashizaki,Y.
Submitssion and Chemission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, UNL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA library"
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Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
/db_xref="FANTOM DB:C230039G09"
/db_xref="taxon:I0090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="C230039G9"
/tissue type="cerebellum"
/clone lib="RIKEN full-length
/dev_stage="0 day neonate"
230. .685
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/procein_id="Bac38599.1"
/db_xref="G1:26349919"
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LAERWSGKKGDIJASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQK
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Division of Experimental Animal Research in Riken prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 1352.8; 99.4%; Pred. No. 0; ative 0; Mismatches
                                                                                                                                 organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sayaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
                   AKO82749

1376 bp mRNA linear HTC 03-APR-2004
Mus musculus ES cells cDNA, RIKBI (M11-langth enriched library,
clone:C330002NO5 produce:1600025D17RIK PROTEIN (FUTATIVE RETINOIC
ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (STREN) Genomic Sciences Center (SSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Genomic Sciences Center and Genome Science Laboratory in RIKEN
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                                                                                                                                                                                                                                                                                   Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                               AK082749.1 GI:26349918
HTC; CAP trapper.
Mus musculus (house mouse)
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1586)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUJ-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-25 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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Nature 409, 685-690 (2001)
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/db_xref="taxon:10090"
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/organism="Mus musculus"
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                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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LOCUS

RESULT 8 AK010702 ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL

ACCESSION VERSION KEYWORDS

(GSC), Yokohama,

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/clone="2410050022"
/cell type="ES cells"
/cell type="ES cells"
/cell type="ES cells"
/cell type="ES cells"
225. 1217
/note="1600025D17RIK PROTEIN (PUTATIVE RETINOIC
ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE)
(SPTR|QDAU1, evidence: FASTY, 100%ID, 100%length,
putative"
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Pred. No. 0;
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Matches 1362; Conservative
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IMAGE 7470381 57, mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheeda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia Laboratory for Genomics and Bioinformatics,
University of Georgia Express Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM15772...
France Library Trow: g column: 19
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I (bases I to 766)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                           GCCAGAGCCACGCCAGAGAGTGCAGAGAGAGCACCTGACCTAACCCCCCTGGAAAGCCAA
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1055 AGCAGCCAGGCCTGCCTCTTCCTTCCACCAAGCATTCTTCTGCTGGTCCTTGTCGGAT
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                                                            GGTAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGGGTGGACGCCAGA
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Seg primer: JENREV (CAGGAAACAGCTATGACC)
High quality sequence stop: 766.
Location/Qualifiers
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/tissue_type="tumor, gross tissue"
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/lab_host="DH108"
/clone_lib="NCI_CGAP_Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                BG974240 1inear EST 12-JUN-2001
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1 (Sess 1 to 766)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                             661 GAAGGGGGACATAGCCTCCCTGGGAGGAAGAATCCAAGAAGAAGAAGCGCAGCGGAGTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10978 row. column: 17
High quality sequence stop: 761.
Location/Qualifiers
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                                                                                                                                     GGGCTCCTCCAGTGGCAGCAGCAGGAGGAAGGAACTGGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:4979944"
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                                                                                                                                                   /clone libe MILL WATE FARE 1: NOLI; Site 2: ECORV; Note="Vector: pExpress-1; Site 1: NOLI; Site 2: ECORV; RNA obtained from human embryonic stem cells Isolated from the inner cell mass of blastocyse stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BGO1. Positive for GATA4, MixLi, MaxLi, HNF4aLpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dT primers 5'-pGACTAGTTCTAGATCGGGGGGGGCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is non-normalized (normalized by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
                                      /tissue type="human embryonic stem cells differentiated to an early endodermal cell type"
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                                                                                                                                  /lab_host="DH10B-T1 phage-resistant E. coli"
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                                                                                     cell type="human embryonic stem cells" cell line="BG01"
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100.0%; Pred. No. 7.7e-179;
ive 0; Mismatches 0;
clone="IMAGE:7470381"
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Matches 766,
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/tissue_type="retina"
/tishost="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye, Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3:3 bb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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llarity 99.2%; Pred. No. 3.4e-175;
Conservative 0; Mismatches 6;
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AGENCOURT_8932400 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6468664
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioceience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM13996 row: i column: 17
High quality sequence stop: 632.
High quality sequence stop: 632.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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           GTGCAGAAAGGCATCGCCCCTCCCACACAGCCCCCCTGATGAGCTGTGTGAGCCCAGCTTAGT
                                                                          GCTCCAGCAAGGACAGCTGTCCCAGCATCAGGTCTCCTCCCTTGGCTGTGCCCCTTTC
                                                                                                                                                                                 CTTCCCTTGAACAACAGCAAGAGGTGGAAGGATCTGGGGTGCTGGGAGACGCCACCCCAA
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                                                      GTCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGACACGCGCACGCGCAGCGCACA
                                                                                                                    GCTCCAGCAAGGACAGCTGCTGTCCAGCATCAGGTCTCCTCCCTTGGCTGTGCCCCTTTC
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/clone="IMAGE:30142422"
/lab host="DH10B (phage-resistant)"
/clone lib="NHH MGC 13"
/note="Vector: pcWVSport6.1; Site_1: EcoRV; Site_2: Not1;
/note="vector: pcWVSport6.1; Site_1: Site_
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0051 row: k column: 07
High quality sequence stop: 609.
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AGENCOURT 11288067 NIH MCC_1135 Mus musculus cDNA clone IMAGE:30142422 5', mRNA sequence.
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone="IMAGE:5035030"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab host="Origin."
/clone=lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pcWV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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602890091F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035030 5'
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1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                        L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbe-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM11097 row: f column: 23
High quality sequence stop: 784.
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Pred. No. 2.5e-173;
0; Mismatches 7; Indels 3;

    .793
    organism="Mus musculus"

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/strain="Czech II"
                                                                                                                                              Mus musculus (house mouse)
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                                                        DB 6;
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Pred. No. 2.8e-171;
0; Mismatches 4;
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                                                                NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Gapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14127 row: h column: 13
High quality sequence stop: 608.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 768)
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/dev_stage="5 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
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/clone="IMAGE:6528637"
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1 (Bases 1 to 892)

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31982623. Incation/Qualifiers
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                                    WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943(
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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/strain="FVB/N"
/db xref="taxon:10090"
/clone="MGC:19340 IMAGE:4222133"
/clone lib="NCI CGAP_Kid14"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:10090"
/cell_line="Pl9; derived from matings between C3H/He females and male animals carrying an X chromosome derived from a feral mouse (McBurney & Rogers, Dev. Biol., 89, 503)"
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Glozak,M.A., Li,Y., Reuille,R., Kim,K.H., Vo,M.N.
Trapping and characterization of novel retinoid re
Mol. Endocrinol. 17 (1), 27-41 (2003)
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Glozak,M.A., Li,Y., Reuille,R. and Rogers,M.B.
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Glozak, M.A., Li,Y., Reuille,R. and kwye
Direct Submission
Submitted (15-MAR-2001) Biology, Univer
E. Fowler Avenue, Tampa, FL 33620, USA
Location/Qualifiers
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Mus musculus mRNA for mFLJ00338 protein.
AK220209
AK220209.1 GI:60359829
FLI_CDNA.

LOCUS DEFINITION ACCESSION VERSION KEYWORDS

RESULT 3 AK220209

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Okazaki,N., Kikuno,R.F., Ohara,R., Inamoto,S., Kitamura,H.,
Nagase,T., Ohara,O. and Koga,H.
Ragase,T., Ohara,O. and Koga,H.
Prediction of the Coding Sequences of Mouse Homologues of KIAA
Gene. The Complete Nucleotide Sequences of Mouse KIAA-homologous
CDNAS Identified by Screening of Terminal sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.

L. Published Only in Database (2005)
2 Chazes 1 to 1655)
3 CAzaki,N., F.Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
L. Submitted (22-FEB-2005) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics, 2-6-7
Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3918)
1 Location/Qualifiers
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VHKGVKVVMDIPYELMNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CDS is predicted by in silico analysis. Start codon is not identified."
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Pred. No. 0;
0; Mismatches 16; Indels 23;
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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/note="vector:modified pBC ?
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="msk03217"
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musculus (house mouse)
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Matches 1629; Conservative C
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| 1594 CCTTTGTCCCCCAATCCCAGGGGCTGGAAGGCCATC 1436 CCTTTGTCCCCCCAATCCCAGGGGCTGGAAGGCCATC 1654 CAGTTACTAGAGGGTGCTGGGAGGGCCCGGGGTTGG 1656 CAGTTACTAGAGGGTGCTGGGAGCGCCCGGGGTTGG 1714 TCAGCCTTCTAACACTGCAGCCCCTTAATACAGTTC 1553TTTCTAACACTGCAGCCCCTTAATACAGTTC 1569 -CACGCCCCCACACACACACATAATTA-TTTCG 1608 GCCCCCCCACACACACATTTTTTCG 1608 GCCCCCCCCACACACACATTTTTTTCG 1608 GCCCCCCCCACACACACATTTTTTTTTTTTTTTTTTTTT | BC008898 Homo sapiens trinucleotide repeat cont MGC:1220 IMGB:2959532), complete cds. BC008898 BC008898. GI:33870484 MGC. Homo sapiens (human) Homo sapiens (human) Homo sapiens Hominidae; Homo. I (bases 1 to 1413) Strausberg, R.L., Feingold, E.A., Grouse Xiausberg, R.L., Collins, F.S., Wagner, L. Altschul, S.F., Jordan, H., Moore, T., Max Diatchenko, L., Marusina, K. Fr., Marusina, R. Buetow, K. H. Biatchenko, L., Marusina, K. Fr., Baratchenko, L., Marusina, K. Fr., Baratchenko, L., Marusina, K., Farmer, A. Stapleton, M., Soares, M. B., Bonaldo, M. F. | Scheetz, T.E., Brownstein, M.J., Usdin, T Carninci, P., Prange, C., Raha, S.S., Log Abramson, R.D., Mallahy, S.J., Bosak, S. Morley, R.D., Malek, J.A., Gunaratne, P Worley, K.C., Hale, S., Garcia, A.M., Gay Villalon, D. K., Muzny, D. M., Sodergren, E Fahey, J., Helton, B., Ketteman, M., Mada Sanchez, A., Whiting, M., Madan, A., Youn Bouffard, G. G., Blakesley, R.W., Tuochma Dickson, M.C., Rodriguez, A.C., Grimwood Butterfield, Y.S., Krzywinski, M.I., Ska Schnerch, A., Schein, J.E., Jones, S.J. a Generation and initial analysis of mor human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), | 12477932 2 (bases 1 to 1413) Strausberg, R. Direct Submission Submitted (29-MXY-2001) National Institute, 20-MXY-2001) National Instigent Collection (MGC), Cancer Genomics Institute, 31 Center Drive, Room 11A03 USA NIH-MGC Project URL: http://mgc.nci.ni On Aug 19, 2003 this sequence version Contact: MGC help desk Email: gapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Labora CDNA Library Preparation: Rubin Labora CDNA Library Preparation: Rubin Labora CDNA Library Presparation: Rubin Labora CDNA Library Presparation: Rubin Labora CDNA Library Arrayed By: The I.M.A.G.E DNA Sequencing by: Institute for Systehtup://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton Madan, Stephanie Rodrigues, Amy Sanche |
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| | | 1054 GGGTGCTGGGAACGGCACCCCAAAGGGAAGAGGAGGAGAGAGA | H—H H—H H—H 4—4 H—H |
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ouse, L.H., Derge, J.G.,
r.L., Shemmen, C.M., Schuler, G.D.,
K.H., Schaefer, C.F., Bhat, N.K.,
Max, S.I., Wang, J., Hath, F.,
A.A., Rubin, G.M., Hong, L.,
M.B., Casawant, T.L.,
Loquellano, N.A., Peters, G.J.,
S.A., McEwan, P.J.,
S.A., McEwan, P.J.,
S.A., McEwan, P.J.,
A.J., Hulyk, S.W.,
en, P.H., Richards, S.,
Gay, L.J., Hulyk, S.W.,
en, E.J., Lu, X., Gibbs, R.A.,
Madan, A., Rodrigues, S.,
Chan, J., Schmutz, J., Myers, R.M.,
wood, J., Schmutz, J., Myers, R.M.,
Wood, J., Schmutz, J., Myers, R.M.,
J. and Marra, M.A. GGTTTGGGGTAATCACTCACTGGCTC 1713 CCTTCTGTTGTGGTGACTCC---- 1768 TCACCATCATTGGAGGCTTAACCTGT 1653 RNA linear PRI 29-JUN-2004 ntaining 5, mRNA (cDNA clone s. ta; Vertebrata; Euteleostomi; ; Primates; Catarrhini; titutes of Health, Mammalian cs Office, National Cancer 03, Bethesda, MD 20892-2590, on, Mark Ketteman, Anuradha hez and Michelle Whiting nih.gov n replaced gi:14286203. , 16899-16903 (2002) ratory .E. Consortium (LLNL) :ems Biology CATGCTGTTCAT 1814

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: m Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
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EL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 691.6; DB 8; Length 1413;
Pred. No. 1.9e-158;
0; Mismatches 139; Indels 6;
                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                 'codon_start=1
'product="trinucleotide repeat containing
                                                                                                /organism="Homo sapiens"
|mol_type="maxNa"
|db_xref="taxon:9606"
|clone="MGC:1220 IMAGE:2959532"
|tissue_type="Colon, adenocarcinoma"
|clone="ib="NIH MGC_15"
                                                                                                                                                                                                               1. .1413
//gene="TNRC5"
/note="Symonyms: ERDA5, CAG4A"
/db_xref="GeneID:10695"
                                                                                                                                                                                                  'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.6%; 284.5%; 1
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Mammaliae; Homo.

It (bases 1 to 1413)

Straubberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collinns,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubhin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gluaratne,P.H., Richards,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,B., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Butterfield,Y.S., Krzywinski,M.I., Skallus,D.E.,
Butterfield,Y.S., Krzywinski,M.I., Skallus,D.E.,
Schnetch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC008961 Homo sapiens trinucleotide repeat containing 5, mRNA (cDNA clone MGC:4122 IMAGE:2959532), complete cds.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                             AGCAGTGTGACGTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC
                                                                                                                          ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGAAAGGACA
                                                                                                                                                                                                                                                       CCAGTTGCCTGGCAGAGCAGTCCGGCAAGAAGAAGACACAGACACAGCTGCCCTGGGAGGAG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                            425 AGGGTATGTCGGAGACCTTTGAGACGCTGCACCTAGTCCACAAAGGGGGTCAAGGTGG
                                                                                                                                CCAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAGGGAGACACAGCACAGCTGCCCTGGGAGGA
319 CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT
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Sequence 135 from Patent WO0140466.
AX464002
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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SOURCE
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AUTHORS
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MOSMPEPASRCLLLLPLLLLLLLPAPELGPSQAGAEENDWVR
LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
ICKRLLDYSLHKERTGSNRFAKGMSETPETLHNLVHKGYKVVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLCANHVLKGKDTSCLAEGWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
EL"
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14286319.
Contact: MGC help desk
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/produc="trinucleotide repeat containing
/prote=in_id="AAH08961.1"
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Pred. No. 1.9e-158;
0; Mismatches 139;
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/gene="TNRC5"
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/gene="TNRC5"
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Hominidae; Homo.

1. (Dases 1 to 1675)

1. (Dases 1 to 1675)

2. (Lark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaten,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.B., Haldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbis,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stingn,J., Vagis,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
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bikkgctyvtyveepeeviedmyrnhqeedlteficannylkgkotsclaeqmsgkkgdt
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El"
                          Homō sapiens (human)
Homo sapiens
Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CA 94080, USA
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Pred. No. 1.9e-158;
); Mismatches 139;
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Submitted (01-AVG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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PRI 03-0CT-2003

1675 bp mRNA linear PRI 03-OCT-Homo sapiens clone DNA88004 CTG4A (UNQ1934) mRNA, complete cds. A7358960

DEFINITION ACCESSION VERSION

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/translation="MOSMPERASRCILLIPLLILLILLIPAPELGPSOAGAEENDWVR
LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
LCKLLDYSLHKERTGSNRFAKGMSETFETLINLVHKGVKVYMDIPYELMNETSAEVA
LCKCLDYSLHKERTGSNRFAKGMSETFETLINLVHKGVKVYMDIPYELMNETSAEVA
ALGGKKGCVLVEEFEEVIEDWYRNHQEEDLTEFLCANHVLKGKDTSCLAEQWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
EL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Action Start Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obl Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: TRAL Plate: 9 Row: o Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalsky, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (12-MR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGGGTCCGGCTGGGCCATGGAGTCCA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/codon start=1
/product="trinucleotide repeat containing
/protein_id="AAH04423.1"
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Pred. No. 1.9e-158;
0; Mismatches 139;
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/db_xref="GeneID:10695"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Matches 791; Conservative (
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Arange, C., Raha, S.S., Loquellamo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Boasak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lulyk, S.W., Villalon, D.K., Walk, Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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Homo sapiens trinuclectide repeat containing 5, mRNA (cDNA clone
MGC:3530 IMAGE:2819660), complete cds.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
     GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTTGCCA
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanezons or transcripts, for detecting expression and other uses
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Patent: WO 02068579-A 2467 06-SEP-2002;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
ICKRLLIIACTRRGPAAIDLPRACQRPLRHYTTWYTKGSRW"
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                                                                       Hominidae; Homo.

1 (bases 1 to 962)

Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S.,
Breschel, T.S., Stine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A.

cDNAs with long CAG trinucleotide repeats from human brain

Hum. Genet. 100 (1), 114-122 (1997)
                                                                                                                                                                                                                                           Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S., Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S., Breschell, T.S., Strine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A. Direct Submission

Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCA 361
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                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGGA
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26.7%; Score 491.2; DB 8; Length 962;
Best Local Similarity 87.3%; Pred. No. 2.8e-109;
Matches 549; Conservative 0; Mismatches 79; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'tissue_type="cerebral cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .962
/organism="Homo sapiens"
/mol_type="mRNN"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAB91442.1"
db_xref="GI:2565063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388. .819
/gene="CTG4a"
/note="polyleucine rich"
/codon_start=1
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/rpt_type=tandem
/rpt_unit="ctg"
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                                                                                                                                                                                                                                                                                             663 CACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGAAG
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                                                                                                                                                                                                Score 484; DB 14;
Pred. No. 1.7e-107;
                                                                                                                                                                                                                                                 0; Mismatches 215;
                                                                                                    188569. 188668 /
estimated_length=unknown
                               /note="wgs_contig"
164279. .166935
/note="wgs_contig"
188569. .188668
                                                                                                                                                                                                26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (199-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:23270097.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                           Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Maylor Plaza, Huuston, TX 77030, USA (bases 1 to 246404) (bases 1 to 246404) Rat Genome Sequencing Consortium.
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Williams, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, J., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Clohe name: CH230-3M14
------ Summary Statistics
Assembly program: Atlas;
Consensus quality: 238268 bases at least Q40
Consensus quality: 240099 bases at least Q30
Consensus quality: 241516 bases at least Q30
Estimated insert size: 241516 bases at least Q30
Batimated insert in Q20 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161257: contig of 161257 bp in length
161357: gap of unknown length
188568: contig of 27211 bp in length
18668: gap of unknown length
246404: contig of 57736 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GBSQ
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/estimated length=unknown
161358. .163910
                                                                                                                                                                                                                                                    Rat Genome Sequencing Consortium.
Direct Submission
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- Genome Center
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JOURNAL
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| 0y 526 GAGGTGGCTGACCTCAAGAAGCAGTGTGACGTGCTGGTGGAAGAGGTTTGAAGAGGTGATT 585 0b 361 GAGGTGGCTGACCTCAAGAACCAGTGTGATGTGCTGGTGGAAGAGTTTGAAGAGGTGATC 420 0y 586 GAGGACTGGTACAGGAACCACCAGGAGGAAGACCTGATTCCTCTGGCCAACCAC 645 1 GAGGACTGGTACAGGAACCACCAGGAGGAAGACCTGACTGA | 98 8 8 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | JOURNAL Patent: US 6607879-A 274 19-AUG-2003; FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers 11534 /organism="unknown" /mol_type="genomic DNA" Ouery Match Query Match 24.9%; Score 458.6; DB 6; Length 1534; Best Local Similarity 84.8%; Pred. No. 2.8e-101; Matches 525; Conservative 0; Mismatches 92; Indels 2; Gaps 2; Oy 5 CGAGGAGGAGAGCCCGCGCGCTCTTTGCTTTGGTCCGCTGGCCTGGTCTGT 123 Oy 65 TGTTGAGCTCGCCCGCTCTTTTGTTCTTTGTCTTCTCTTCTCTCTCTCTCTCTTCT |
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| Db 24146 TTTGGTTTGGGTCCTCTCAGCCTCCAGAGTGCCCCCCCTTTTC 24205 Oy 1592 TGCCTTTGTCCCCAATCCCAGG-GCTGAAGGCTATTGGAGGCTTAAC 1649 Db 24206 TGCCTATGTCCCCAAGTCCAGGAAGGCTGTCATTGGAGGCTTAAC 24265 Oy 1650 CTGCCATTGTCCCCCAGGTCCTGGAAGGCTGTCATTGGAGGCTTAAC 24265 Oy 1650 CTGCCAGTTACTAGGAGGTGCTGCATGGATGGTTT 1692 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | RESULT 12 AR379595 LOCUS LOCUS DEFINITION Sequence 140 from patent US 6607879. ACCESSION AR379595 1 G1:40087229 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. AUTHORS COCKS, B.G., Stuart,S.G. and Seilhamer,J.J. Unclassified. AUTHORS TITLE RESPONSE Gene expression JOURNAL LOCATION/Qualifiers LOCATION/Qualifiers LOCATION/Qualifiers SOURCE LOCATION/Qualifiers LOCATION/LYPE="Genomic DNA" | Query Match 25.4%; Score 467; DB 6; Length 1201; Best Local Similarity 79.0%; Pred. No. 2.4e-103; Agenth 1201; Best Local Similarity 79.0%; Pred. No. 2.4e-103; Agenth 1201; Matches 612; Conservative 0; Mismatches 95; Indels 68; Gaps 2; 228 GCTGAAGTCGGCTTTTGGGGAAGGGAAGGCAAGGAGTGATTGACCGGCTATGG 60 Qy 228 GCTGAAGTCGGCTTTGAGGAACCAAGACCAAGGAGTGATTGACCGGCTATGG 60 Qy 288 CATCCTGGACGAGGGGTCTGAAGTCAAGTACACAAGAGCTAATTCAGATCCCCCAGG 120 Qy 28 CATCCTGGACGAGAGGGTCTGAGGTCAATACAACAAGTCCATTTCAGATCCCCCAGG 120 Qy 330 121 CCAGATGACCTATCCTTCCAGGTCTGAGTCACTTCCATTGGGGTTAAT Qy 346 GAAGTCACTGAGACCATTTGCAAGAGCTCTGGACTACGGCTCCACAAGAGAGACT Qy 346 GAAGTCACTGAGACCATTTGCAAGAGGTCTCTGGATTATAGCCTGCACAAGAGAGACC Qy 346 GAAGTCACTGAGACCATTTGCAAGAGGTCTCTGGATTATAGCCTGCACAAGAGAGACC Qy 346 GAAGTCACTGAGACCATTTGCAAGAGGTCTCTGGAACTTTAAGACCTGCACAAGAGAGCC Qy 406 GGCAGCAACGGTTTTGCCAAGGGTTTTTGCAAGAGCTCTTTGAGACCTTTCAGACTTACACTACTCTTAA Db 241 GGCAGCAATCGATTTGCCAAGGGTTTTGAGACCTTTTGAGACTTTCAGAACTGCTAA Db 241 GGCAGCAATCGATTTGCAAGGGTTTTGAGACTTTTGAGACTTTCAGA CACAAAAGGGTCAAGGTTTTGCAAGATTTCCCATTGAGACTTTTGAGACTTTCAGA CACAAAAGGGTCAAGGTTTTGAGACTTTTAAGACTTTTGAGACTTTTCAGA |

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: n Column: 9.
Location/Qualifiers
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: am@@bcm.tmc.edu
Gontact: am@@bcm.tmc.edu
Gontact: B. H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Pred. No. 4.4e-101;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/clone="lmAGE:3457829"
/tissue type="Cerrix, carcinoma"
/clone lib="NIH MGC_12"
/lab_host="DH10B"
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Is Strausberg, L. Peingold, E. A., Grouse, L. H., Derge, J. G., Klausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. L., Collins, F. S., Wagner, L., Shemmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K. Barmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Schersfrih, M. J., Usdin, T. L., Schersfrih, S. J., Bosak, S. A., McEwan, P. J., McEwan, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Rabey, J., Helton, E. Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y. Butterfield, Y. S., Krzywinski, M. I., Skalaka, U., Smailus, D. E., Schnutz, J., Myers, R. M., Schein, J. E., J. Sanchezh, S., Krzywinski, M. I., Skalaka, U., Smailus, D. E., Schnerch, A., Schein, J. E., J. and Marra, M. A. Chenthon, J. M., Green, E. D., Schnerch, A., Schein, J. E., J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (22-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                   TTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGGACCGGCAGCAATCGATTTGC
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          TGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTATGGCATCCTGGACCAGAA
                                                                            GGGCTCTGGAGTCAAGTACAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCAT
                                                                                                                  TTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTTGC
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was selected for full length sequencing because passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                   /mol_type="mRNA"
/db_xrefe=taxon:9606"
/clone="MAGE:3609644"
/tissue_type="Uterus, endometrium adenocarcinoma"
/clone_lib="NHM MGC 44"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.9%; Score 457.8; DB 8; Length Best Local Similarity 81.6%; Pred. No. 4.4e-101; Matches 544; Conservative 0; Mismatches 117; Indels
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he : 9087 secs
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                                                                            Location/Qualifiers
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I (bases 1 to 1593)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Rlauener, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., K., Gibbs, R.A., Fahey, J., Helton, E., Garcia, A.M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bulterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

N. Parcs, Matl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                            ברעות אפל 1593 pp mRNA linear PRI 25-JUN-2004
Homo sapiens trinuclectide repeat containing 5, mRNA (cDNA clone
IMAGE:3609644), partial cds.
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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Series: IRAL Plate: 27 Row: f Column: 20
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Mammalia; Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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On Dec 19, 2003 this sequence version replaced gi:15079962.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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BC011767.2 GI:40226374
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Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trinucleotide repeat protein; TRP; T243; embryonic stem cell; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine trinucleotide repeat protein (TRP) cDNA sequence.
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ALIGNMENTS

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ADA84507 ADB29763 ADA80291 ADA75533 ADA46758 ADB25054

ADA93230

Allen KD;

Cells comprising a heterozogous merings of producting a comprising a heterozogous merings of producting a knockout mouse comprising a heterozogous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozogous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fraggle X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to anodel both the pathogenic mechanism and the trinucleotide repeat instability in the mouse describes methods of producing embryonic stem (ES) trinucleotide repeat protein The present sequence encodes for (TRP). The invention describes me

Sequence 1839 BP; 424 A; 522 C; 535 G; 358 T; 0 U; 0 Other;

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120 180 240 240 300 360 420 480 900 9 420 540 540 99 180 300 360 480 900 720 720 TCCATGTCTGAGCTCGCGCCCCCGCTGCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTG 120 9 TTTGAGGAAACGGGAAAGACCAAGGAATTGACACCGGCTATGGCATCCTGGACGGG gecacgaggaggaagcgcccgccccccrcrcrcrcrcggrccggcrcggcraggg TCCATGTCTGAGCTCGCGCCCCCCTTTTTTTCCTTTGCTGCTGCTTCGCTG CTGCTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGGCTGAGGAGACCGACTGG CTGCTCCTTCCTGCCCGAAGCTAGGCCCGAGTCCCGCGGGGGCTGAGGAGAGACCGA GTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCT GTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGCTGTGGAGCTGAAGTCGGGCT TTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGG AAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC AAGGGCTCTGGAGTCAAGTACAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC **ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGAGTGGCAGCAACCGGTTT** ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGAGGAGGACTGGCAACCGGTTT GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAG GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAG GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTC GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGG AAGAAGCAGTGTGACGTGCTGGTGGAAGAGTTTTGAAGAGGTGATTGAGGACTGGTACAGG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGTGAAGGGGAAAG GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGA GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGAAGGAGGGGACATAGCCTCCCTGGGA Gaps ö DB 4; Length 1839; 0; Indels Query Match
100.0%; Score 1839;
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| QQ | 721 | dogaagaaaticcaagaagaagagagagagagagagagaagacag | 780 |
| δ | 781 | CAGAGGAAGGAACGAAGGCCTGGGGGGAGATGCCAACGCCGAGGAGGAGGAGGAGGTGTG | 840 |
| qq | 781 | CAGAGGAAGGAACTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGGTGTG | 840 |
| <i>&</i> 4 | 841 | 841 CAGAAGGCATCGCCCCTCCCACACACCCCCCTGATGAGCTGTGAGCCCAGCTTAGTGT 900 641 CAGAAGGCCATCGCCTCCCACACACACACCCCTGATGAGCTGTGAGCCCAGCTTAGTGT 900 641 CAGAAGGCCATCGCTTCACACACACACACACACACACACA | 006 |
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| දු දි | 901 | CTTGMATCMAGACCCCTGMACTTCMAGACTTGGGAACACGCAACACGCAACACAACA | 096 |
| ìò | 961 | CCAGCAAGAACAGCTGCTCCAGCATCAGGTCTCCTTCCCTTGGCTGTGCCCCTTTCCTT | 1020 |
| g g | 961 | CCAGCAAGGACAGCTGCTGTCCAGCATCAGGTCTCCCTTGCTGTGCCCCTTTCCTT | 1020 |
| ٥'n | 1021 | CCCTTGAACAACAACGAGGAGGGAAGGGATCTGGGGGTGCTGGGAGACGGCACCCCAAAGG | 1080 |
| ΩÞ | 1021 | CCTTGAACAACAACAAGAAGGATGTAGGGATGTTGGGGTGCTGGGAAGGCACCCCAAAGG | 1080 |
| à | 1081 | GAAGAGGAGGAGGAGCAGCTCTTTTCTACACAGTCCCCCTCACGAGCTCCGG | 1140 |
| Op | 1081 | GAAGAGGAGGAGCAGCACTCTTTCTACACAGTCCCCTCACGAGCTCCGG | 1140 |
| λ̈́O | 1141 | GGTCCACCCAGCATCCCCAGGTGAGATCCAGGCTCCTGACATGGAAGCTGAAGAGCATG | 1200 |
| Db | 1141 | GGTCCACCCAGGCTGAGGTCCAGGCTCCTGACATGGAAGCTGAAGAGCATG | 1200 |
| ογ | 1201 | AGGCACATAAGATGCTCACCAGCGCCCCTTCAGCCAGGAAGAACTCCGTGCAGCTCAG | 1260 |
| Db | 1201 | Addeacataadargeteaceageeeeeerreageeaggaaggaeereeggeeeeereag | 1260 |
| λ̈́O | 1261 | CAGCCAGGCTGCTTTCCTTCCACCAAGCATTCTTCTGCTGGTCCTTGTCGGATGG | 1320 |
| ΟÞ | 1261 | CAGCCAGGCCTGCCTCCTTCCACCAAGCATTCTCTTCTGCTGGTCCTTGTCGGATGG | 1320 |
| δγ | 1321 | TAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGCACAAAAGGGGGCTGGACCCCAGAGC | 1380 |
| Db | 1321 | TAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGGCACAAAGGGGGCTGGACGCCAGAGG | 1380 |
| δλ | 1381 | CAGAGCCACGCCAGAGACTGCAGAGAGGCACCTGACCTCCCCCTCGAAAGCCAATC | 1440 |
| Dβ | 1381 | CAGAGCCACGCCAGAGACTGCAGAGAGGCCACCTGACCTAACCCCCCTGGAAAGCCAATC | 1440 |
| ò | 1441 | TGCAGTICCCGTGCCACCCACTCCTGAGGACGCCTCATGCTCTGCCCCAGCCCTTCT | 1500 |
| q _Q | 1441 | TGCAGTTCCCGTGTCCACCCACTCCTCCTGAGACGCCTCATGCTCTGCCCCAGCCCTTCT | 1500 |
| ò | 1501 | CCCAGGGCTACCAGAGTAAACACCTTTTTGGCCTTTTCGGTTTTGGTTCCTCGTCTCATCA | 1560 |
| Ор | 1501 | CCCAGGGCTACCAGAGTAAACACCTTTTGGCTTTTGGTTTCCTTGGGTCCTCATCA | 1560 |
| λ̈́o | 1561 | GCCTCCAGAGIGTCCCCTCATCGATCTTTTTTGCCTTTGTCCCCCCAATCCCAGGGGCTGG | 1620 |
| Ор | 1561 | GCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCTTTGTCCCCAATCCCAGGGGGCTGG | 1620 |
| ò | 1621 | AAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGCGAGCGCC | 1680 |
| ΩÞ | 1621 | AAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGGAGCGCC | 1680 |
| ٥٧ | 1681 | CGGGGTTGGTTTGGGGGTAATCACTCACTGCTGTCTACCTGCTACTGCGCCCCTTA | 1740 |
| qq | 1681 | cddddirddiriadddiaarcactcactddcictcadccrictaacactdcagccccria | 1740 |
| δλ | 1741 | ATACAGTTCCTTCTGTTGTGGTGACTCCCACGCCCCCACACACA | 1800 |
| ор | 1741 | ATACAGTTCCTTCTGTTGTGGTGACTCCCACGCCCCCACACACA | 1800 |

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C gene. The T243 gene encodes for a trinuclectide repeat protein (TRP). The invention describes methods of producing embryonic steem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding TRP, where the disruption in a gene encoding TRP, where the disruption in a gene encoding TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout course. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
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Pred. No. 0;
                                                                                                                                                                                  Trinucleotide repeat protein; TRP; T243; embryonic stem cell; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.
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Allen KD;
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55. .894
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Best Local Similarity

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72. .902
/*teg= a /*teg= a /product = "protein involved in FGF signal transduction"
         CCCCAAAGGGAAGAGGAGGAGCAGAAGGCAGCTCTCTTTCTACACAGTCCCCCTCAC
                   GAGCTCCGGGGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTG
                                                      GAGCTCCGGGGTCCACCCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATGGAAGCTG
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The present sequence encodes a protein involved in fibroblast growth factor (FGF) signal transduction. Such proteins are useful for analyzing the mechanism of formation of various organs, such as midbrain optic-tectum portion by a midbrain mesencephalon border, the mechanism of formation of cerebellum. mechanisms of formation of inner ear, blood vessels, limb buds, teeth, and canceration mechanisms of a cell.
                                                                                                                                                                                                                                                                                                                                                                    Novel gene encoding protein involved in fibroblast growth factor signal transduction, useful for analyzing mechanism of formation of organs such as midbrain optic-tectum portion, cerebellum, inner ear and canceration mechanism of cell.
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ive 0; Mismatches
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01-JUN-2004; 2004WO-JP007910
                                                                    05-JUN-2003; 2003JP-00161005
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Matches 1528; Conservative
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ACA54677 standard; cDNA; 1378

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The present invention relates to the isolation of human nuclear factor-
kappaB (NP-kappaB) associated polypeptides and polynucleotides. The NP-
kappaB associated polypeptide and polynucleotide sequences are useful for
preventing, treating or ameliorating various disorders including immune
cdisorders, inflammatory disorders, cancers, disorders relating to
aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
cd Asematopoletic tumours, hyper-IgM syndromes, hypolidrotic ectodermal
dysplasia, x-linked anhidrotic ectodermal dysplasia, immunodeficiency,
cd papalasia, x-linked anhidrotic ectodermal dysplasia, immunodeficiency,
cminontinentia pigmenti, viral infections (e.g. those caused by human
cc incontinentia pigmenti, viral infections (e.g. those caused by human
cc immunodeficiency virus (HIV), human T-cell lymphotropic virus (HILV),
chepatitis B, hepatitis C, Epstein Barr virus (EBN), influenza),
crheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental
atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental
cc allergic encephalomyelitis (EAE), autoimmune disorders, infection, hyperproliferative disorders related to aberrant squal
cc responses, hypercongenital conditions, birth defects, necrotic lesions,
creanding cardivascular disorders, diseases of the panoreas
cc disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial
cinfections, cardiovascular disorders, infertility, psoriasis and
chaemolytic anaemia. The present sequence represents a human NF-kappaB
cascoiated polymucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infertility; psoriagis; haemolytic anaemia; antiinflammatory; anti-HIV; cytostatic; hepatotropic; virucide; antirheumatic; antiarthritic; antiasthmatic; immunoomodulator; antidiabetic; antiallargic; neuroprotective; immunosuppressive; vulnerary; antibacterial; antiinfertility; antianaemic; antipsoriatic; cerebroprotective; cardiant; antiarteriosclerotic; gene; ss.
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                                                                                                                                                                       cancer;
                                                                                                                                                               nuclear factor-kappaB; NF-kappaB; immune disorder;
                                                                                          Human NP-kappaB associated polynucleotide sequence #117
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26-APR-2001; 2001US-0286645P.
09-JAN-2002; 2002US-0346986P.
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                                 Length 1378
Sequence 1378 BP; 311 A; 399 C; 419 G; 249 T; 0 U; 0 Other;
                                   Score 691.6; DB 10; Length
Pred. No. 6.4e-168;
); Mismatches 139; Indels
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84.5%;
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Nuclear factor kappa B; NFkappaB; inflammation; cardiovascular disease; neoplasm; gastrointestinal disease; immune disorder; immune deficiency; dermatological disease; infection; nutritional disorder; cerebrovascular ischemia; endocrine disease; injury; respiratory disease; gynecology and obstetrics; kawasaki disease; rheumatic fever; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding an NFkappaB associated molecule, useful for diagnosing, preventing, treating, or ameliorating a medical condition, e.g. cancer, wounds, or immune, inflammatory, hepatic, viral or pulmonary disorder.
                                                                                                                                                                                                            Human trinucleotide repeat containing 5 protein, cDNA.
                                  ВР.
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                                  ADU83175 standard; cDNA; 1378
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                                                                                                                                                    (first entry)
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Claim 1; SEQ ID NO 139; 646pp; English.

The invention relates to an isolated nucleic acid molecule having

NrkappaB (nuclear factor kappa B) modulating activity (or its fragments,
variants, homologs and sequences hybridizing to it.) Also included are an
isolated polypeptide capable of modulating an NrkappaB response (or its

Comain, epitope, variant, species homolog or interacting protein), an
isolated antibody that binds specifically to the isolated polypeptide, a
method for preventing (retaring) or ameliorating) a medical condition, an
isolated antibody that binds specifically to the isolated polypeptide, a
method for diagnosing a NrkappaB associated condition (or a susceptibility

CC diagnosing a NrkappaB associated condition) (or a subject, a method for
identifying a binding partner to the polypeptide, a method for identifying
a compound that modulates the biological activity of a NrkappaB

CC f modulating the biological activity of a NrkappaB

CC condition, e.g. immune disorder, an inflammatory disorder related to

CC disorders Hodgkins lymphomas, hematopoietic tumors, hyperial bepatits CC

CHAPLY, HTW-1, hepptids B

CC disorders Hodgkins lymphomas, hematopoietic tumors, hyperial activity,

CC disorders, immunodeficiency, al inflammatory disorder related to hypohydrotic ectodermal dysplasia, and related to hypohydrotic ectodermal dysplasia, and related to hyperial activity, and evenion of immune eigenchers, incrotic lease

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propagation in cells infected with other viruses, associated with EL-8, disorders associated with aberrant IL-8 expression, disorders associated with aberrant IL-8 activity, pulmonary disorders, pulmonary fibrosis, Behcet's disease, bacterial infections, gynecological diseases, psoriasis, IgA nephropathy, chronic obstructive pulmonary disease, Kawasaki disease, Crohn's disease, peripheral arterial occlusive disease, Hodgkin's disease, idiopathic intermediate uveitis, hyaline membrane disease, acute rheumatic fever, chronic Theumatic heart disease, ulcerative colitis, autoimmune disorders, and autoimmune thyroid disease. The present sequence encodes a protein found to interact with the NFkappa
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                                                                                                                                                                                                                                                                        / Match 37.6%; Score 691.6; DB 14; Length 1378; Local Similarity 84.5%; Pred. No. 6.4e-168; nes 791; Conservative 0; Mismatches 139; Indels 6;
                                                                                                                                                                                                                                      Sequence 1378 BP; 311 A; 399 C; 419 G; 249 T; 0 U; 0 Other;
                                                                                                                                                                                                    modulating protein AD037
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         Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                  Human cDNA sequence encoding for PRO4409 polypeptide
                                  934
                                  TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                             CTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA
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                                                                                               AAS21311 standard; cDNA; 1675
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99US-0170262P.
99WO-US030095.
99WO-US030911.
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Human, PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
                                                                                                                                                                                                                             779 AGCAGAGGAAGTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAGGTGG
                                                               ACCAGGAGGAAGACCTGACTTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA
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                                                                                                                                                                                                                                                                                                                         AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to calls expressing PRO polypeptides, to adulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, polypeptide expression in a cell sample tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proliferation cartilage, the proliferation of inner ear utricular supporting cells or of T-colliferation of inner ear utricular supporting cells or of T-colliferation of inner ear utricular supporting cells or of T-colliferation of solve and of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor villa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The probes, antiesness encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The probes, antiesness encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The probes, antiesness encoding PRO polypeptides can be used in assays to identify molecules.
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                                                                                                                                                                                  Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.
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                                          Deforge L, Desnoyers L, Filvaroff E, G,
,, Godowski PJ, Gurney AL, Sherwood S;
umas D, Watanabe CK, Wood WI, Zhang Z;
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                       Baker KP, Beresini M, Deforge L
Gerritsen ME, Goddard A, Godows
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking polypeptides are useful for detecting other PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for contentifying agonists or antagonists. The PRO polypeptides are useful for contentifying agonists or antagonists. The PRO polypeptides are useful for contentifying adouted the properties of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the prosesce of tumours. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generic analysis of individuals with encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence of useful an electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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             20-JUN-2001; 2001WO-US019692.
21-JUN-2001; 2001WS-0088-W19.
22-JUN-2001; 2001WG-US020116.
29-JUN-2001; 2001WO-US021166.
09-JUL-2001; 2001WG-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
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587 CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT 646
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                                  GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGAGCTGGCAGCAACCGGTTTGCCA 424
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                                                                                                                                                ACCAGGAGGAAGACCTGAATTCCTCTGTGCCAACCACGTGCTGAAGGAAAGGACA 664
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                                                                                                                                                                                                                                AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG
                                                                                                                           TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA
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encodes a novel human PRO protein
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2001US-00866028
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Gerritsen ME, Goddard A,
Smith V, Stéwart TA, Tum
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P-PSDB; ABU59718.
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18-MAY-2001; 2
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01-JUN-2001;
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25-MAY-2001;
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29-JUN-2001;
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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in comparing a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cuseful for treating cardiac insufficiency disorders. PRO154 and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO439, PRO826, PRO439, PRO826, PRO439, PRO826, PRO439, PRO826, PRO439, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO439, PRO186 or PRO535, PRO6335, PRO826, PRO4397 induce c-foe in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating concerous tumours. PRO812 inhibits vascular collocated in growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mamnas which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO826, PRO1068 or PRO1132 enhance survival proliferation of cretinal neurons cells (PRO1132 is also enhances survival/proliferation of decreased mesangial cell function such as Berger disease or other comphropathies associated with dermatitis, herpetiforms or other comphropathies associated with dermatitis, herpetiforms or other comphropathies associated with dermatitis, herpetiforms or control disease. PRO1100, PRO844, PRO1112, PRO1192 and PRO1137 induce the condises a novel human PRO PROFE in judices, and core in the proventing special processed mesangial cells injuries, and arthritis. This sequence Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis. 3 Gao Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

245 AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGAAGG 304 346 406 TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGACCGACTGGGTGC 184 466 244 526 364 646 424 484 AGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGGTCAAGGTGG 544 rearegacarcecerareaecreresaaceaecacacreereseaecreeresecreaecae 604 664 TGCAGAAGGCATCGCCCCTCCCACACCCCCCCTGATGAGCTGTGAGCCCCAGCTTAGTG 898 64 TGTCTGAGCTCGCCCCCCCCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC GCCTGCCCAGCAAATGCGAAGTGTGAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG 725 AGAAATCCAAGAAGAAGCGCAGCGGAGTCAAG-----GGCTCCTCCAGTGGCAGCAGCA 779 AGCAGAGGAAGTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGTG 587 CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT 647 GCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGGAGCGGCAGCAATCGATTTGCCA GATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTTGCCA AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGGACTGGTACAGGAACC ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCA AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAAGGGGTTGA TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA 9 Length 1675; 37.6%; Score 691.6; DB 8; Length 84.5%; Pred. No. 7e-168; ive 0; Mismatches 139; Indels cercrierecreadaceceridaririrga acercadada 1222 899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA Query Match 37.6 Best Local Similarity 84.5 Matches 791, Conservative 665 1127 1187 Ŋ 65 347 125 407 185 467 305 365 425 707 167 545 827 605 485 839 a ઠે g ò 셤 ઠે 셤 ò 셤 δ 셤 ò a ઠ g ò g 8 g ò g à g ò 유 g ò ò 셤

RESULT 9 ACD41862 ID ACD4:

Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;

ACD41862 standard; cDNA; 1675 BP

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The invention relates to an isolated nucleic acid comprising at least 80 sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequences given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 PRO4978, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
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P-PSDB; ABO24908.
plood;
                                                               Human; 88; gene; PRO; secreted protein; transmembrane protein; tumour; cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; bloc proteoglycan; cartilage; cytokine; peripheral blood monouclear cell; pBMC; glucose uptake; FRA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell; A-peptide; factor VIIA.
                                                Human secreted/transmembrane protein (PRO) cDNA #68.
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2000WO-US004342
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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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20-DEC-1999;
20-DEC-1999;
                                                                                                                                              Homo sapiens.
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15-SEP-1999;
15-SEP-1999;
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10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
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07-0CT-1998;
29-0CT-1998;
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20-NOV-1998;
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000US-00747259.
2000WO-US034956.
2001US-00796498.
2001WO-US006520.
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2001US-00802706
2001US-00808689
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2001US-00854208
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2001US-00872035.
2001WS-00874503.
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2001US-00886342.
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2000WO-US022031.
2000WO-US022031.
2000WO-US023522.
2000WO-US03338.
2000WO-US030952.
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2000WO-US007377.
2000WO-US007532.
                                                                  2000WO-US008439.
2000WO-US013705.
2000WO-US014042.
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28-FEB-2001;
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Culture Collection (ATCC) Accession Numbers listed in the specification also included are a vector comprising the novel nucleic acid, a host cell also included are a vector comprising the novel nucleic acid, a host cell also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a RPO polypeptide, the isolated RPO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO compressing a RPO polypeptide, including at least one biological activity of a cell expressing a RPO polypeptide, stimulating the release of tumnour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononiciear cells (PBMC)), andipocyte cells of proliferation of or gene expression in pericyte cells, stimulating the proliferation of respective cells (or proliferation of or gene expression in pericyte cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells (or of T-lymphocyte cells, or of atumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polymucleotide is useful in molecular biology, in generating antisense RNA and DNA, and in gene therapy. The combinant techniques, and in generating either transgenic animals or recombinant techniques, and in generating either transgenic animals or recombinant techniques, and in generating either transgenic animals or responsive to the polympeptide or antibody, such as the propertice or antibody, such as the present of antibody, such as the present of an entipody, such as the present of antibody, such as the present cent antibody, such as and in preparing a medicament for treating a condition and and and an entipody is used in preparing a medicament for treating a condition and an angent and an antipode antibody.
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specification, or of the DNA deposited under any of the American Type
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                                                                     887 ACCAGGAGGAAGACCTGACTGAATTCCTCTGCGCCAACCACGTGCTGAAGGGGAAAAGACA 946
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                827 AGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTGTACAGGAACC
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                                               ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA
                                                                                                AGAAATCCAAGAAGAAGCGCAGCGGAGTCAAG------GGCTCCTCCAGTGGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 88; gene; secreted protein; transmembrane protein; PRO; inflammatory disease; organ failure; atherosoclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication;
 545 AGCAGTGTGACGTGCTGGTGGAAGAGTTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC
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18-JUL-2001; 2001US-00908827. 06-AUG-2001; 2001US-00924419. 09-AUG-2001; 2001US-00927796. 16-AUG-2001; 2001US-00931836. 2001WO-US021735 19-DEC-2001; 2001US-00028072 (GETH) GENENTECH INC 09-JUL-2001;

3 Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Gerritsen ME, Goddard Smith V, Stewart TA, Baker KP,

WPI; 2003-331925/31. P-PSDB; ABU66913.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 135; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 27% nucleotide sequences, encoding the corresponding PRO polypeptide (one of 27% secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under american Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, and mature sequences, methods of detecting PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for simulating the release of TNF-alpha (tumour contrace) factor alpha) from human blood, (and the proliferation of chondrocyte cells, the proliferation of contraction of confidences, methods of inner ear urticular supporting cells, the catriage, proliferation of finer ear urticular supporting cells, the catriage, proliferation of finer cells, the release or protecyly proliferation of conduction of inner ear urticular supporting cells, the catriage, proliferation of conduction of inner ear urticular supporting cells, the cells, a method for inhibiting the proliferation of proliferation of finer modulating the uptake of glucose or free cartiage, proliferation of cattor vills, or the differentiation of adprocyte cells, a method for modulating the uptake of glucose or free calls, a method for detecting the presence of a tumour in a mammal and olygomucleotide probe derived from any of the nucleic sequences cells, and polypeptides are useful for treating of the inventions of infammatory diseases, organ failure, atherosclerosis, cardiac injury, intendeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both cuestul in tissue typing. The present sequence encodes a PRO protein

Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;

346 466 406 TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGGCGGGCTGAGGAGACCGACTGGGTGC 184 64 407 TGCTGCCGGCCCCGGAGCTGGGCCCGAGCCGGAGCTGAGGAGAACGACGACTGGGTTC CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGGCCATGGAGTCCA 347 recerebadecedederecederetrativarienterrationalistation Gaps 9 37.6%; Score 691.6; DB 8; Length 1675; 84.5%; Pred. No. 7e-168; ive 0; Mismatches 139; Indels 6; Best Local Similarity 84.5 Matches 791; Conservative 65 125 Ŋ Query Match 셤 g 셤 à 8 ò

185 GATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG 244

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29-OCT-1998;
29-OCT-1998;
20-NOV-1998;
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14-SEP-1998
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02-JUN-1999
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   1006
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Tumour necrosis factor alpha release; TNF-alpha release;
Jucose uptake modulator;
cell proliferation stimulator; PRA uptake modulator;
cell differentiation stimulator; cytokine release stimulator; tumour;
lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
                                                              586
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                                                                                                                                        424
                                                                                                                                                                                                                                                                                          AGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGCTGATTGAGGACTGGTACAGGAACC 604
                                                                                                                                                                                                                                                                                                        ACCAGGAGGAAGCCTGACTGAATTCCTCTGCGCCAACCACGTGTGAAGGAAAAGACA 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAGAGGAAGGAACTGGGGGGCCTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGGTG 838
                                                                                                                                                      GCCTGCCCAGCAAATGCGAAGTGTGTGTAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG
                                      AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGGAAGG
                                                         527 AGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGCTATGGCATCCTGGACCAGAAGG
                                                                                       GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT
                                                                                                     587 CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT
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                                                                                                                                       GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGAGCTGGCAGCAACCGGTTTGCCA
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25-MAY-2001; 2001US-00860216.
25-MAY-2001; 2001US-00866028.
35-MAY-2001; 2001US-00866034.
35-MAY-2001; 2001WO-US-00866034.
                         28-FEB-2001; 2001US-07796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
                                                     2001US-00808689.
2001US-00816744.
       2000WO-US032678.
2000US-00747259.
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2001US-00854280.
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2001US-00886342.
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2001US-00927796
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10-NOV-2000; 2
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20-DEC-2000; 2
28-FEB-2001; 2
28-FEB-2001; 2
01-MAR-2001; 2
                                                     14-MAR-2001;
22-MAR-2001;
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10-MAY-2001;
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(GETH) GENENTECH INC.

Gao W; Deforge L, Desnoyers L, Filvaroff E, Gz A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Baker KP, Beresini M, De Gerritsen ME, Goddard A, Smith V, Stewart TA, Tum

WPI; 2003-584997/55. P-PSDB, ADA45655

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 135; 659pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (1) is useful for stimulating the cransmembrane) polypeptides (1). (1) is useful for stimulating the cransmean blood, for modulating the uptake of glucose or FRA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner are utricular supporting cells, for stimulating the proliferation of inner are utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for stimulating proliferation of endothelial cells, for detecting cells, for stimulating proliferation of endothelial cells, for detecting the prosence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (1) is also useful as therapeutic agent. RNO is useful in the corresponding in the corresponding of interaction of properties from mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals which in turn are useful in the development and concomme identification, as chromosome anaker, and for generating chromosome identification, as chromosome serum, and for generating chromosome identification, as chromosomes or serum, and for generating chromosome identification, as chromosomes or serum, and for generating to a constance of the present of the pre

| 8888 | affinity purificat: sources. (I) and (; a novel human secre | ion of PRO from recombinant cell culture or natural [11] are useful for tissue typing. This sequence encodes eted and transmembrane PRO polypeptide. |
|-------------------|---|--|
| 80 | Sequence 1675 BP; | 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other; |
| M B C | uery Match est Local Similarity atches 791; Conserv | 37.6%; Score 691.6; DB 9; Length 1675; / 84.5%; Pred. No. 7e-168; .vative 0; Mismatches 139; Indels 6; Gaps 1; |
| 8 8 | 5 CGAGGGAGGAAGCGCC | |
| 3 8 | s TGT | CCGCTGCTCTTATTCCTTTGCTGCTGCTTCCGCTGCTGC 12. |
| Dβ | 347 TGCCTGAGC | CTGAGCCCGCGTCTCCTTTTTTTTCCTTGCTGCTGCTGCTGCTG |
| δ | Ē- | |
| QQ | CTGC | ACTGGGTTC 46 |
| දි දි | 185 GATTGCCCP 467 GCCTGCCC | CCAGCAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG 244 |
| à | 'n | 304 |
| q | 527 AGGAAACCC | |
| ठे ह | 90 | GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT 364 |
| a a | 20 | CACIGAGACCAIII 04 |
| કે ક | 365 GCAAGAGGC | GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAAGGACTGGCAGCAACCGGTTTGCCA 424 |
| 8 | . 25 | AGGGGTCAAGGTGG 48 |
| 연 | 0.7 | |
| ð í | 95 | TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGGAGGTGGCTGACCTCAAGA 544 |
| <u>a</u> | . 9 | 20 MONACOUNT |
| දි සි | 545 AGCAGTGTC 827 AGCAGTGTC | CAGIGIGACGIGCIGGAAGAGITIGAAGAGGIGAITICAGGACIGGIACAGGAACC 604 |
| ò | 605 ACCAGGAGC | ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGACGGAAAGGAAAGAACA 664 |
| qq | 887 ACCAGGAGG | crececeaaccacereaaecaaaaaaaaa 9 |
| à | 65 | 47 (|
| В | 947 CCAGTIGCO | GGGAGGGA 10 |
| ζο q ₀ | 725 AGAAATCC 1007 AGAAGTCC | AGRAATCCAAGAAGAAGCGCAGCGCAGTCAAGGGCTCCTCCAGTGGCAGCAGCA 778 |
| ò | 779 AGCAGAGG | CCAAC |
| q | 1067 AACAAAGG | CCGAGGAGG |
| ò | 839 TGCAGAAGC | GCAGAAGGCATCGCCCCTCCCACACAGCCCCCTGATGAGCTGTGAGCCTATAGTG 898 |
| qq | 1127 TCCAGAAGG | scarcecereteacacacadadececerdateacreteadececacer 1186 |
| ò | 1 66 | 34 |
| QQ | 1187 cérciére | creadaccccrearitrgaagcreadda 1222 |

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tumour necrosis factor-alpha, TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FRA; skeletal muscle cell; adipooyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
                                                                             Human; gene; 88; PRO; secreted polypeptide; transmembrane polypeptide;
                        ADA76085 standard; cDNA; 1675 BP
                                                                                                                                                                                                                                  98WO-US018824.
98WO-US019093.
98WO-US019094.
                                                                                                                                                                                                                                                                               98WO-US022991.
98WO-US022992.
98WO-US024855.
98WO-US025108.
99WO-US000106.
                                                                Human PRO polynucleotide #68.
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98WO-US019330.
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98WO-US021141
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99WO-US010733
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99WO-US020111
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99WO-US020944
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99WO-US021547
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99WO-US031274
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                                                  (first entry)
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30-DEC-1999;
05-JAN-2000; 2
                                                                                                                                                     Homo sapiens
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02-JUN-1999;
01-SEP-1999;
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15-SEP-1999;
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                                      ADA76085;
             RESULT 12
                  ADA76085
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2001US-00866028.
2001US-00866034.
2001WC-US017092.
2001US-00872035.
2001US-00874503.
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2001US-00927796.
2001US-00931836.
2001US-00028072.
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2001US-00808689.
2001US-00816744.
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2001US-00886342.
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2001US-00796498
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2001US-00887879
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20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
                                                    22-MAY-2000;
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02-JUN-2000;
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3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-687639/65. P-PSDB; ADA76086 New isolated nucleic acid encoding a secreted and transmembrane polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 135; 659pp; English

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The invention relates to alorated human PKU polypeptides lescreted and transmembrane polypeptides an antibody which specifically binds to a PRO invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for catering the proliferation or differentiation of chondrocyte cells and a method for catering the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polypuroleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polyprocides may also actisense RNA and DNA and in gene therapy. The polyprocides may also be used in preparing PRO polypeptides by recombinant techniques and in capenating at the development and screening of therapeutically useful and the development and screening of therapeutically useful and medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of or gene expression in periove cells, for remulating differentiation of adipocyte cells, for stimulating checked or stricular cartial of sendentels cells or adipocyte cells, for inducing endothelial cell tube formation and for treating checked proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell to repeace and proceed proliferation of associated sporter related joint problems, arthritis. PRO polypeptides which stimulate the release of proteoglycans from arthritis. PRO polypeptides which stimulate such as various mammalian haemoglobin-cells may benefit from enhanced local immune system cell infiltration. This sequence represents
invention relates to isolated human PRO polypeptides (secreted and
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Gaps 9 DB 9; Length 1675; Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other; Score 691.6; DB 9; Length Pred. No. 7e-168; 0; Mismatches 139; Indels Query Match Best Local Similarity 84.5%; Matches 791; Conservative

646 706 992 287 cecesesaceaacceccestricerrassercesseccessecardearricaa 346 406 184 466 244 526 304 586 364 424 484 TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA 544 TGTCTGAGCTCGCGCCCCCGCTGCTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC 64 GCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTT CGAGGGAGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAGTCCA 347 ráccidadecedederecederáreireirerrecerideriderideraderederede TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGAACCGACTGGGTGC GATTGCCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTGAAGTCGGCTTTTG GecreeceAgeAarteceAagrereraAarararigerigreeAgereAagereage AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGAAGG CCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGGTTAATCGAAGTCACTGAGACCATTT GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGACTGGCAGCAACCGGTTTGCCA GCAAGAGCTCCTGGATTATAGCCTGCACAAGGAGAGAGGACCGGCAGCAATCGATTTGCCA AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG AGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGGGTCAAAGGTGG 305 / 185 245 527 587 365 647 425 707 485 125 407 467 ß 65 g ద g 8 6 ò 유 ò g ò ð 셤 ò ò g 8

98WO-US025108 99WO-US000106

AGAAGTCCAAGAAGAAGAAGCAGCAAGGCCAGCAGGAGGCAGGAGTAGCAGCAGCA 1066 1067 Aacaaaddaaddadchddchrdadddaddccccdaddaddaddaddad 1126 946 AGCAGAGGAAGGAACTIGGGGGGCCTTGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGTG 838 TGCAGAAGGCATCGCCCTCCCACACACCCCCCTGATGAGCTGTGAGCCCAGCTTAGTG 898 664 724 604 886 rearceacerecectarcacercrescaaccacerecrecacaccacacerecececececeace Human, gene, ss, PRO, secreted polypeptide, transmembrane polypeptide, tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung, colon; breast; prostate; rectum, cervix; liver; tumour; cancer; glucose uptake; FFA, adipocyte cell; pericyte cell; proteoglycan; cartilage; inner ear utricular supporting cell; cytokine; A-peptide; accaddaddaddcrdaarrccrcrdcdcaaccacgrdrgaadddaaaaaada 605 ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAAGGACA AGCAGTGTGACGTGCTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACC AGAAATCCAAGAAGAGGGCAGCGGAGTCAAG------GGCTCCTCCAGTGGCAGCAGCA 1187 cérciérecrgádácécérdárirrgaágérgadda 1222 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934 factor VIIA; endothelial cell. 98WO-US012456. 98WO-US014552. 98WO-US017888. ADA18735 standard; cDNA; 1675 Human PRO polynucleotide #68. 98WO-US019330 98WO-US022991 98WO-US022992 2002US-00141755 98WO-US018824 98WO-US019093 98WO-US019094 98WO-US019177 98WO-US019437 98WO-US021141 98WO-US024855 (first entry) US2003054517-A1. 08-MAY-2002; 14-SEP-1998; 14-SEP-1998; 16-SEP-1998; 20-NOV-1998; 01-DEC-1998; 05-JAN-1999; Homo sapiens 1998; 1998; 20-NOV-2003 31-MAR-1997 12-JUN-1998 -SEP-1998 SEP-1998 20-MAR-2003 1998 947 767 545 827 887 999 725 1007 779 839 1127 ADA18735; AUG-10-SEP-RESULT 13 ADA1873 ò 셤 g 셤 ð 셤 ð 셤 ò 셤 ò ò ò

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99WO-US021547
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28-FEB-2001;
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16-DEC-1999;
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22-DEC-1999;
30-DEC-1999;
                 02-JUN-1999;
01-SEP-1999;
08-SEP-1999;
13-SEP-1999;
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06-JAN-2000;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the problemation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are consected in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating suese RNA and DNA and in chromosome and gene mapping, in generating suesting PRO colon, propertides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the coloppeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for crating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for as tumours, for modulating the uptake of glucose or PRA by adipocyte cells, for stimulating the proliferation of inner ear urricular cartilage, for stimulating the proliferation of cygne expression in pericyte cells, for stimulating the release of proteoglycans from PROC cells, for stimulating the release of cycchines from PROC cells, for stimulating the proliferation of inner ear urricular continibiting the differentiation of adipocyte cells and for stimulating the proliferation of supporting the proliferation of supporting a human PRO proliferation of endothelial cells. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent consideration of construction of construction of the propertion of the propertion of the propertion of t
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y AL, Sherwood S;
Wood WI, Zhang Z;
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Pred. No. 7e-168;
0; Mismatches 139; Indels 6;
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A, Godowski PJ, Gurney A
Tumas D, Watanabe CK, Wo
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                                     2001WO-US020116
2001WO-US020106
2001WO-US021735
2001US-00924419
2001US-0092419
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84.5%;
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Matches 791, Conservative
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29-JUN-2001;
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18-JUL-2001;
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16-AUG-2001;
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30-NOV-1999;
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01-DEC-1999;
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02-MAR-2000;
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17-SEP-1998;
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Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inhibitor; cytokine release stimulator; tumour;
und tumour; broast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; chromosome mapping; gene mapping;
gene therapy; chromosome identification; chromosome marker.
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                                                                       CCTCTGGAGTCAAATACACCCAAGTCGGACTTGCGGTTAATCGAAGTCACTGAGACCATTT 646
                                                                                                   GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGGACTGGCAGCAACCGGTTTGCCA 424
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                   AGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGGAAGG 304
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GCCTGCCCAGCAAATGCGAAGTGTGAAATATGTTGCTGTGGAGCTGAAGTCAGCCTTTG 526
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2001US-00796498.
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2001US-00887879.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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                  23-AUG-2000;
24-AUG-2000;
10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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20-DEC-2000;
20-BEC-2000;
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10-MAY-2001;
18-MAY-2001;
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05-APR-2001;
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25-MAY-2001;
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22-JUN-2001;
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Gao Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;

2003-695892/66

P-PSDB; ADA61359

New PRO nucleic acid and encode polypeptides, are useful for manufacturing a medicament for diagnosing or treating cancer

Claim 2; Fig 135; 660pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the proliferation of or gene expression in pericyte to mulating the proliferation of Inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating cells, for stimulating proliferation of endothalial cells, for stimulating proliferation of endothalial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour is lung, colon, breast, constants probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in an assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or reparation of animals or recompany.

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Section Contract

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knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This sequence encodes
                                                                                                                                                                                                                                                      CGCGGGAGGAGCACCGCCCGGTCCTTTAGGGTCCGGGCCCGGCCCGTCCATGGATTCAA 346
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                                                                                                                                                             Score 691.6; DB 9; Length 1675;
Pred. No. 7e-168;
                                                                                                                                  Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;
                                                                                                     a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                           0; Mismatches 139; Indels
                                                                                                                                                                37.6%;
84.5%;
                                                                                                                                                                          Local Similarity
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Claim 2; Fig 135; 660pp; English
1127 TCCAGAAGGCATCCCCTCTCACACACACCCCCTGATGAGCTCTGAGCCCCACCAGCAT 1186
                                                                                                          Human; secreted and transmembrane protein; PRO; gene; ss;
Tumour necrosis factor alpha release; TNF-alpha release;
glucose uptake modulator; FPA uptake modulator;
cell proliferation stimulator; cell differentiation stimulator;
cell differentiation inihibitor; cytokin.
                                                                                               Novel human secreted and transmembrane protein PRO4409 cDNA
                    1187 CCTCTGTGAGACCCCTGATTTTGAAGCTGAGGA 1222
            899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934
                                                         ADB19143 standard; cDNA; 1675 BP
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99WO-US005106.
99WO-US005190.
99WO-US006115.
99WO-US010733.
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16-SEP-1998;
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Novel secreted and transmembrane PRO polypeptides useful for stimulating the release of tumor necrosis factor alpha and detecting the presence of
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FPA by skeletal muscle cells or adiporyt
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                                                                                                             Query Match 37.6%; Score 691.6; DB 9; Length 1675; Best Local Similarity 84.5%; Pred. No. 7e-168; Matches 791; Conservative 0; Mismatches 139; Indels 6;
                                                                                Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 U; 0 Other;
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Db 1187 CCTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA 1222
Search completed: December 29, 2005, 23:12:47
Job time: 1059 secs

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TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 030137
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Seguence 274, App
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1: /cgn2 6/ptodata//ina/1_COMB.seq:*
2: /cgn2 6/ptodata//ina/5_COMB.seq:*
3: /cgn2 6/ptodata//ina/6A_COMB.seq:*
4: /cgn2 6/ptodata//ina/6B_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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| | 25 | 46.4 | 2.5 | 64309 | с | 0S-09 | -949- | 016-1 | US-09-949-016-14581 US-09-949-016-12147 | | Sequence | 14581, | 44 |
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| | 30 | 45 | 2.4 | 474 | m | US-09 | -621- | 976-1 | 18033 | | Seguence | | |
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| ٠. | NOMBE | NUMBER OF SEQUENCES | COENC | ES: 1 | 1508 | | | | | | | | |
| ٠. | CORRE | CORRESPONDENCE ADDRESS | E P | DRESS: | | | | | | | | | |
| | ADDI | ADDRESSEE: | | INCYTE PHARMACEUTICALS, | ARMA | CEUTIC | ALS, | INC. | | | | | |
| | STRI | Ë | 174 P | 3174 PORTER DRIVE | DRIV | œ | | | | | | | |
| ٠. | CITY: | | OALT | o | | | | | | | | | |
| ٠. | STATE: | | CALIFORNIA | NIA | | | | | | | | | |
| | COCT | COUNTRY: 1 | USA | | | | | | | | | | |
| | ZIP: | 94304 | 4 | | | | | | | | | | |
| | COMPUTER | TER REA | DABLE | READABLE FORM: | | | | | | | | | |
| . • | MED | MEDIUM TYPE: Floody disk | | Joppy | disk | | | | | | | | |
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| | APPI | APPLICATION NUMBER: | N N | BER: | | | | | | | | | |
| ٠. | FIL | FILING DATE: | ເລ | | | | | | | | | | |
| ٠. | CLA | CLASSIFICATION: | TION: | | | | | | | | | | |
| | ATTOR | _ | NI IN | FORMAT | : ON | | | | | | | | |
| •- | NAME: | | ler, | Zeller, Karen J | | | | | | | | | |
| ٠. | REG | REGISTRATION NUMBER: | PN NO | MBER: | 37, | 071 | | | | | | | |
| ٠. | REFI | REFERENCE/DOCKET NUMBER: | DOCKE | T NUMB | ER: | PA-0001 | 01 US | | | | | | |
| . | TELEC | TELECOMMUNICATION INFORMATION: | ATION | INFOR | MATI | No | | | | | | | |
| . •• | TEL | TELEPHONE: | (650) | 0) 855 | 855-0555 | r. | | | | | | | |
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APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES: 1808
ADDRESSE: INCTF PHARMACEUTICALS, INC.
STREET: 3174 FORTER DRIVE
                                                                              228 GCTGAAGTCGGCTTTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGG
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                       25.4%; Score 467; DB 3; I
llarity 79.0%; Pred. No. 4.1e-109;
Conservative 0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 274, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
                                     Best Local Similarity
Matches 612; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGGAGGAAGCGCCGCCCGGTCCGCTCTGCGTCCGGCTGGGCCATGGAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 idecitéadecededecedererererererereres recentations de la reconstruction de la reconstruct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 CTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGCCGACTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 CGATTGCCCCAGCAAATGCGAAGTGTGCAAGTATGTTGCTGTGGAGCTG-AAGTCGGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 458.6; DB 3;
Pred. No. 6.3e-107;
); Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA-0001 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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84.8%;
                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.8
Matches 525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: BRSTNOT07
CLONE: 1298861
PALO ALTO
CALIFORNIA
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339 GTTAATTGAAGTCACTGAGACCATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGA 398
                                                                   255 deriggaagagecerragagaarrrargreagecegarecregacraragrerreagecrea 314
                                                                                                                        399 GAGGACTGGCAGCAACCGGTTTGCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAA 458
                                                                                                                                                                  315 gcgcaagggcrcacrgagarargccaagggrcagagrcagaccarggcaacacrgaaagg 374
                                                                                                                                                                                                                        CCTAGTCCACAAAGGGGGTGGTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGAC 518
                                                                                                                                                                                                                                                          435 cagcerceaecercaracercaeaaecaerereaeaecercercereereeaecerreraeae 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 catrorogagacrigeráctrocaccarcarcages 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             639 CAACCACGTGCTGAAGGGAAAGGACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAA 698
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US-09-163-285-1

US-09-163-285-1

Sequence 1, Application US/09163285

Sequence 1, Application US/09163285

Patent No. 6204013

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran

TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            519 CTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTGACGTGCTGGTGGAAGAGGTTTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,285
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,35
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: MANDERER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INPORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
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STRANDEDNESS: single
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1140 GGTGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGACTCAA 1199
                                                                              200 GAAGCAGTGTGTGTGCTGGTGGAGGTTTGAGGGGGGTGATCGAGGACTGGTACAGGAA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 GGCTGAGGAGACCGACTGGGTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 GGAGGAGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 CACAGAGCTACAGGCGGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGG 194
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                                                    543 GAAGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 744;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCFTGARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,285
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTONNEY/AGENT INFORMATION:
NAME: MANDARGOURSE: AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: MNI-049
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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Pred. No. 6.9e-31;
0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    Sequence 3, Application US/09163285
Patent No. 6204013
GENERAL INFORMATION:
                                                                                                                                                     603 CCACCAGGAGGAAGACCTG 621
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Best Local Similarity 57.3%;
Matches 310; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 28 State Stree
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-09-163-285-3
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US-09-163-285-3
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US-09-482-273-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 CAACCACGTGCTGAAGGGAAAGGACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAA 698
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                                                                                                                                                                                                                                                                                                                                                                                             199 GGAGGAGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 TGTGGAGCTGAAGTCGGCTTTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 cacadadciacadededaacidagtededededegicearciceadaddigcigdagerede 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CTATGGCATCCTGGACGGGAAGGGCTCTGGAGTCAAG---TACACCAAGTCGGACTTACG 338
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                                                                                                                                                                                                                                          3
                                                                                                                                                            Length 1512;
                                                                                                                                                       Similarity 57.3%; Score 160.2; DB 3; Length Similarity 57.3%; Pred. No. 9e-31; L0; Conservative 0; Mismatches 228; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT PILING DATE: 2000-01-13
EARLIER PILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 267
SOFTWARE: PARENTIN VET. 2.0
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Patent No. 6534631
    CDS
125..868
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US-09-482-273-23/c
                                                                                                                                                            Query Match
Best Local Simi:
Matches 310;
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LENGTH: 1658
; NAME/KEY:
; LOCATION:
US-09-163-285-1
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                                            Gaps
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  Length 1658;
                                                                                           668 GTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGGACATAGCCTCCCT
                                               Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
8.5%; Score 156.6; DB 3;
76.2%; Pred. No. 7.8e-30;
tive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ATTLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                            902 TIGAATCAAGACCCCTGACTICAGAGCTIGGGA 934
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14/c
; Sequence 14, Application US/08232463
: Petent No. 5670367
; EBNERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                 Conservative
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ADDRESSEE: Foley & La
    Query Match
Best Local Similarity
Matches 208; Conserv
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1465 CTCCTGAGGACGCCTCATGCTCTGCCCAGCCCTTCTCCCAGGGCTACCAGAGTAAACACC 1524
  484
425 AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG
                                                                        485 TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA
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3.1%; Score 56.2; DB 2; Length 7
Best Local Similarity 7.2%; Pred. No. 0.00058;
Matches 31; Conservative 222; Mismatches 180; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSE:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PILING DATE:
PILING DATE:
PILING DATE: 26-046-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PATENTIN RAIN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                   ; Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: pTZgpt-F18
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                                                                                                                                                                                                                                                   RESULT 8
US-08-232-463-14
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TELEX: 89
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US-08-232-463-14
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR PLIING DATE: 2000-10-03
PRIOR PLIING DATE: 2000-09-08
PRIOR PLIING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOTHARE: FRESEQ for Windows Version 4.0
LENGTH: 24207
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                                                    Query Match 4.1%; Score 75.2; DB 2; Length 7218; Best Local Similarity 7.2%; Pred. No. 8.2e-09; Matches 32; Conservative 241; Mismatches 169; Indels 0.
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12-09-949-016-14364/c
; Sequence 14364, Application US/09949016
; Patent No. 6812339
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CCATION: (1)...(24207)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14364
; CLONE: pTZgpt-F1s
US-08-232-463-14
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                       GAGGAGGAGGAGGTGTGCAGAAGG
                                                                                                              ; Sequence 2, Application US/09130114; Patent No. 5976807; GENERAL INFORMATION:
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                                                                                                     US-09-130-114-2/c
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                                                                  TTTTGGCCTTTCGGTTTGGTTCCTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCATCGA 1584
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APPLICANT: HOTLICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEFSION 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)._(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Epstein Barr Virus
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US-09-249-585A-4
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RESULT 11
US-09-949-016-5779
is Sequence 5779, Application US/09949016
j Fatent No. 6812339
j GENERAL INFORMATION:
j PAPLICANT: VENTER, J. Craig et al.
j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
j FILE REPERENCE: CL00130,
j CURRENT APPLICATION NUMBER: US/09/949,016
j CURRENT PILING DATE: 2000-04-14
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APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Evantyotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 0.00055;
0; Mismatches 206;
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New York
: U.S.A.
Best Local Similarity
Matches 181; Conserv
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US-08-728-323A-1
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JERNERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAFESE FARESEQ for Windows Version 4.0
SEQ ID NO 17521
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                  PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5779
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  APPLICATION NUMBER: 60/241,755
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Best Local Similarity 47.3
Matches 181; Conservative
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; ORGANISM: Human
US-09-949-016-5779
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US-09-949-016-17521
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2.7%; Score 49.4; DB 3; Length 87734;

Query Match

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60363 CCACCAGGAGAACATGGGCTAATGGACAACTGGAAATCCAAGCTGGACTCGCTGGCCT
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APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Bdelman, Isidore S.
APPLICANT: Bdelman, Isidore S.
APPLICANT: More Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi,
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0575/52268/JPW/MSC/SKS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
ilarity 47.3%; Pred. No. 0.082;
Conservative 0; Mismatches 201;
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STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60663 ACTGGCGGCCCAGCTGGAGGTG 60685
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; Patent No. 5948676
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
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2481 GCAGGAGCAGGAGTTAGAGGAGCAGGAGCTTAGAGGAGCAGGAGGTGGAAGAGAGA 2540
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Pred. No. 0.038;
0; Mismatches 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squence 1, Application US/09410399; Squence 1, Application US/09410399; Patent No. 648287; GENERAL INFORMATION: APPLICANT: Robertson, Erle S. TITLE OF INVENTION: Methods to Inhibit or E; TITLE OF INVENTION: to Genomic Host DNA; TITLE OF INVENTION: to Genomic Host DNA; CURRENT APPLICATION NUMBER: US/09/410,399; CURRENT FILING DATE: 1999-10-01; NUMBER OF SEQ ID NOS: 6
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Matches 194; Conservative
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US-09-410-399-1
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US-09-410-399-1
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SEQ ID NO 1
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1999-04-21
EARLIER PILING DATE: 1998-11-19
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO 3.
                                                                                                                                                                                                                                                                         446 AGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGC
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Pred. No. 0.038;
0; Mismatches 204; Indels 3.
                                                                                                                                                                                Score 48.6; DB 2; Length 3489;
Pred. No. 0.038;
0; Mismatches 204; Indels 3
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US-09-298-568-1
Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
                                                MOLECULE TYPE: DNA (genomic) FEATURE:
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Best Local Similarity 48.4%;
Matches 194; Conservative
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                                                                                                                                                                                Query Match
Best Local Similarity 48.4°
Matches 194; Conservative
         single
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    STRANDEDNESS:
TOPOLOGY: lin
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COCATION:
US-08-728-323A-1
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1: /cgn2_6/ptodata/1/pubpna/USO2_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
5.1.6
Compugen Ltd
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US-10-431-096-135

US-10-1028-072-135

US-10-123-904-135

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Listing first 45 summaries
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Pred. No. 6.6e-197;
0; Mismatches 139;
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CORGANISM: Homo sapiens
US-10-126-103-139
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GCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGAGGACCGGCAGCAATCGATTTGCCA
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                Score 691.6; DB 7;
Pred. No. 6.6e-197;
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                37.6%;
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Matches 791; Conservative
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US-10-028-072-135
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TITLE OF INVENTION: PACKNOCIED AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
TITLE OF INVENTION: PATHWAY
CURRENT APPLICATION NUMBER: US 60/284,962
PRIOR PILING DATE: 2001-04-19
PRIOR PAPLICATION NUMBER: US 60/284,962
PRIOR PILING DATE: 2002-04-19
PRIOR PAPLICATION NUMBER: US 60/286,645
PRIOR PAPLICATION NUMBER: US 60/386,645
PRIOR PAPLICATION NUMBER: US 60/346,986
PRIOR PAPLICATION NUMBER: US 60/346,986
PRIOR PAPLING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/346,986
PRIOR APPLICATION NUMBER: US 60
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Publication No. US20040086896A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-01-33
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PRIOR FILING DATE: 1998-02-04
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PRIOR PELICATION NUMBER: 60/074086
PRIOR APPLICATION NUMBER: 60/074092
PRIOR APPLICATION NUMBER: 60/074092
PRIOR PILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR PRILING DATE: 1998-03-27
PRIOR PRILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07963
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PRIOR APPLICATION NUMBER: 60/081818
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PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/083545
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PRIOR APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/063755
APPLICATION NUMBER: 1997-10-17
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APPLICATION NUMBER: 60/069334
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APPLICATION NUMBER: 60/069694
FILING DATE: 1997-12-16
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APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695
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APPLICATION NUMBER: 60/084627
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FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/066511
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CURRENT APPLICATION NUMBER: US/10/028,072
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PRIOR APPLICATION NUMBER: 60/05974
PRIOR PILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/062814
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
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FILING DATE: 1997-10-29
Publication No. US20030004311A1
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Gerritsen, Mary E
Goddard, Audrey
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                                                       Baker, Kevin P.
Beresini, Maureen
DeForge, Laura
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Laura
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gaodward, Audrey
APPLICANT: Gadward, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Shewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
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APPLICANT: Watanabe, Colin K
APPLICANT: Anang, Zemin
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APPLICANT: Zhang, Zemin
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Pred. No. 7.1e-197;
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       R APPLICATION NUMBER: 60/08523

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

DR APPLICATION NUMBER: 60/08539

R FILING DATE: 1998-05-13

R FILING DATE: 1998-05-13

DR FILING DATE: 1998-05-15

DR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                            DR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/088730

PR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/088741

PR FILING DATE: 1998-06-10

PR FILING DATE: 1998-06-10

PR FILING DATE: 1998-06-10

PR FILING DATE: 1998-06-10

PR PLICATION NUMBER: 60/088858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089947

R APPLICATION NUMBER: 60/090349

R APPLICATION NUMBER: 60/090429

R APPLICATION NUMBER: 60/090429

R APPLICATION NUMBER: 60/090429

R APPLICATION NUMBER: 60/090445

R APPLICATION NUMBER: 60/090445

R APPLICATION NUMBER: 60/090445
                                                                                                                                                                                                                                                                                                                                                                                                                R FILING DATE: 19/98-06-11

R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089599

R APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090863
                                                                                                                                                                                                                                   PILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
                                                                                                                                                                                                         FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086430
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84.5%;
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Best Local Similarity 84..-
Local 791; Conservative
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APPLICANT: Baker, Kevin P.
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US-10-121-049-135
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Best Local Simi:
Matches 791;
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US-10-121-049-135
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LENGTH: 1675
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                                                                                                                                                     Score 691.6; DB 5;
Pred. No. 7.1e-197;
0; Mismatches 139;
TITLE OF INVENTION: ACIDS ENCODING THE SAME PILE REFERENCE: P3330R10182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
PRIOR APPLOACATION removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
                                                                                                                                                      Query Match 37.6%;
Best Local Similarity 84.5%;
Matches 791; Conservative
                                                                                                                  ORGANISM: Homo Sapien
US-10-140-808-135
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Danie A.
APPLICANT: Tumas, Danie A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Construction A.
APPLICANT: Construction A.
APPLICANT: ALIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/121, 049
CURRENT APPLICATION NUMBER: 2002-04-12
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                                                                                                      ccrcrercagaccccraarrrrgaaccrgaga
                                                                  TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                                                                                                                                                                                        ; Sequence 115, Application US/10121049; Publication No. US20030022239A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                              Beresini, Maureen
DeForge, Laura
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Filvaroff, Ellen
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Gerritsen, Mary
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RESULT 7
US-10-140-470-135
; Sequence 135, Application US/10140470
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GCAAGAGCTCCTGGATTATAGCCTGCACAAGGAGAAGGACCGGCAGCAATCGATTTGCCA
                         AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGGTCAAAGGTGG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
CURRENT FILING DATE: 2002-04-16
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Publication No. US20030022328A1
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
Tumas, Daniel
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Wood, William
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Filvaroff, Ellen
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CORGANISM: Homo Sapien
US-10-123-904-135
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US-10-123-904-135
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Pred. No. 7.1e-197;
0; Mismatches 139;
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ilarity 84.5%;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FITLE OF INVENTION: ACCOUNT THE SAME
FILE REPERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
                  605 ACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACA
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84.5%; Pred. No. 7.1e-197;
iive 0; Mismatches 139; Indels 6;
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Sequence 135, Application US/10175746
Publication No. US20030027270A1
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Smith, Victoria
Stewart, Timothy A.
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Gerritsen, Mary E
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L.
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Matches 791, Conservative
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APPLICANT: Goddard, Audrey B.
APPLICANT: Goddwski, Paul J.
APPLICANT: Gorney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Shewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin K.
APPLICANT: Zhang, Zemin K.
APPLICANT: AND INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3339RICLEO
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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Pred. No. 7.1e-197;
0; Mismatches 139;
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84.5%;
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Baker, Kevin P.
Beresini, Maureen
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Best Local Similarity 84.5
Matches 791; Conservative
                                           DeForge, Laura
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US-10-140-470-135
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LENGTH: 1675
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Query Match 37.6
Best Local Similarity 84.5
Matches 791; Conservative
                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapien
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                     TCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGCCGACTGGGTGC
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US-10-176-918-135
IS-10-176-918-135
Publication US/10176918
Publication No. US20030027275A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: Berorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goodard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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APPLICANT: Sherwood, Steven
APPLICANT: Scwart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: ARANGEMEN SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 2333012038
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
FILE OF SEQ ID NOS: 550
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
FILE OF TATA
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84.5%; Pred. No. 7.1e-197;
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APPLICANT: Tumae, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
                                                                                                                                                                                                        GCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTTGCCA
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                              1007 AGAAGTCCAAGAAGAAGAGCAGCAGGCCAAGGCAGGAGGGGGGAGTAGCAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1628B
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NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                               CCTCTGTCCTGAGACCCCTGATTTTGAAGCTGAGGA 1222
                                                                                                                                                                                                                                                                                                                                                     899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA 934
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Pred. No. 7.1e-197;
0; Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 135, Application US/10176921
Publication No. US20030027276A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-06-20
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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84.5%;
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DeForge, Laura
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; ORGANISM: Homo Sapien
US-10-176-921-135
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LENGTH: 1675
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Best Local 3
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APPLICANT: GOGGELY, PRUIT J.
APPLICANT: GUTNEY, AUSTIN L.
APPLICANT: GUTNEY, AUSTIN L.
APPLICANT: STEWART, TIMOCHY A.
APPLICANT: STEWART, TIMOCHY A.
APPLICANT: TIMOS, Daniel
APPLICANT: Tumos, Daniel
APPLICANT: Tumos, Daniel
APPLICANT: Tumos, Daniel
APPLICANT: Wood, William
APPLICANT: WOOD, William
APPLICANT: Chang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
PRIOT APPLICATION THE SAME
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 15-75
FILE TOWN AND ACIDS TOWN AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 TGTCTGAGCTCGCGCCCCCTCTTATTTCCTTTGCTGCTGCTGCTTCCGCTGCTGC
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Pred. No. 7.1e-197;
0; Mismatches 139;
                         TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
                                                                                                                                                                                                            ; Sequence 135, Application US/10140474; Publication No. US20030032156A1; GENERAL INFORMATION:
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Best Local Similarity 84.5%;
Matches 791; Conservative 0
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Filvaroff, Ellen
Gao, Wei-Oiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Peul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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ORGANISM: Homo Sapien
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US-10-140-474-135
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                    CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
                                                                                                                                                                                                                                                                         Query Match 37.6%; Score 691.6; DB 5; Best Local Similarity 84.5%; Pred. No. 7.1e-197; Matches 791; Conservative 0; Mismatches 139;
CURRENT APPLICATION NUMBER: US/10/137,865
                                                                                                                                                              TYPE: DNA
CORGANISM: Homo Sapien
US-10-137-865-135
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APPLICANT: Beresini, Mauren
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gac, Wei-Qiang
APPLICANT: Gacinesh, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Scewart, Timothy A.
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: ARBINON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCENETED
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/142, 431
CURRENT APPLICATION NUMBER: US/10/142, 431
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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; Publication No. US20030036179A1
; GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Perrore, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Wei-Qiang
APPLICANT: Geoviei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Guddard, Audrey
APPLICANT: Gudowski, Paul J.
APPLICANT: Sherwood, Steven
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ORGANISM: Homo Sapien
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Pred. No. 7.1e-197;
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US-10-143-114-135
Sequence 135, Application US/10143114
Publication No. US20030036180A1
GENERAL INFORMATION:
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1067 AACAAAGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCCCAGCCCCGAGGAGGATGAGGGCA 1126
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C244
CURRENT APPLICATION NUMBER: U5/10/142,419
CURRENT APPLICATION NUMBER: U5/10/142,419
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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; Sequence 135, Application US/10142419
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBENCE: P3330R.C211
CURRENT APPLICATION NUMBER: US/10/143,114
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
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84.5%; Pred. No. 7.1e-197;
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ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR PILING DATE: 1997-06-26
PRIOR PELING DATE: 1997-09-17
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Sequence 1, Appl
Sequence 11, Appl
Sequence 181, Appl
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US-11-186-284-3
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US-10-928-446A-181
US-10-928-446A-183
US-10-928-446A-187
US-10-928-446A-189
US-10-928-446A-191
US-10-928-446A-195
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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Maximum DB
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Sequence 55, Appl.
Sequence 13415, A
Sequence 13233, A
Sequence 8, Appl.
Sequence 52971, A
Sequence 455, App
Sequence 455, App
Sequence 453, App
Sequence 24, Appl
Sequence 637, App
Sequence 59, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
                                                                                                                                                                                                                                                                                                        Sequence 13424, A
Sequence 13245, A
Sequence 5006, Ap
US-10-995-561-55
US-10-995-561-13415
US-10-995-561-1323
US-11-061-869-8
US-10-750-185-52971
US-10-750-185-6060
US-10-995-561-455
US-10-995-561-455
US-10-995-561-455
US-10-995-561-455
US-10-995-561-455
US-10-995-561-455
US-10-995-561-4637
US-11-121-086-44
US-11-069-834-59
US-11-069-834-51
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ALIGNMENTS

APPLICANT: Desnoyers, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gaodwark, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Shewart, Timothy A.
APPLICANT: Shewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REFERENCE: P3330RICLE
CURRENT FILING DATE: 2002-04-24 Sequence 135, Application US/10131826A publication No. US20050245730A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen APPLICANT: DeForge, Laura

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                 - See File Wrapper or PALM
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                                                                                                                                                                                    Indels
                                                                                                                                                Query Match 37.6%; Score 691.6; DB 6; Best Local Similarity 84.5%; Pred. No. 7.6e-169; Matches 791; Conservative 0; Mismatches 139;
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
                                                                                 TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                      , ORGANISM: HOMO
US-10-131-826A-135
                                                                   LENGTH: 1675
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US-11-121-086-5
Sequence 5, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138 6000-00000
CURRENT APPLICATION NUMBER: 05/50/50
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
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US-10-750-185-37066

US-10-750-185-37066

Sequence 37066, Application US/10750185

Publication No. US20050260603A1

GENERAL IRPORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
TILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TILE TILING DATE: 2003-12-31
CURRENT APPLICATION NUMBER: US 60/437,482
FRICK APPLICATION NUMBER: US 60/437,482
PRIOR PELING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 37066
TENTIOR PATENTIN VERSION 3.1
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2.7%; Score 48.8; DB 7; Length 1
Best Local Similarity 43.9%; Pred. No. 0.029;
Matches 258; Conservative 0; Mismatches 327; Indels
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                     DB 6;
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Pred. No. 1.9e-17;
0; Mismatches 21
899 TCCTTGAATCAAGACCCCTGACTTCAGAGCTTGGGA
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nilarity 84.8%;
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Best Local Similarity
Matches 117; Conserv
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US-10-750-185-37066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adammani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: WHERE: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 49
                                                                                                                                     703 GACATAGCCTCCCTGGGAAGAAATCCAAGAAGAAGCGCAGCGGAGTCAAGGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
   APPLICANT: Labat, Ivan
; APPLICANT: APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
                TGTGCCAACCACGTGCTGAAGGGAAAGGACACGAGTTGCCTAGCAGAGCGGTGGTCTGGC
                                                                                                           AAG----AAGGGGGACATAGCCTCCCTGGGAGGAAGAAATCCAAGAAGAAGCGCAGCGGA
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Pred. No. 1.4;
0; Mismatches 113;
                                                                                                                                                                                                                                                                                             GATGCCAACGCCGAGGAGGAGGAGGGTGTGCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/10821234; Publication No. US20050255114A1; GENERAL INFORMATION:
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48.9%;
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ORGANISM: Homo sapiens
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Matches 108; Conserv
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AGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGGAAGGGCTCTGGAGTCAAGTACA
                                                                                        323 CCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACCATTTGCAAGAGCTTCTGGACT
                                                                                                                                  .4652 AACAGGTGCTAGGACACTGTGGGGACGTCCCAGATGCCAGGGGCAGTGGAGACAGGAGGA
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APPLICANT: NIESERN, KIRSTEN V.
TITLE OF INVENTION: UNCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PILING DATE: 2004-05-04
PRIOR PLING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
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Pred. No. 1.2;
0; Mismatches 174; Indels
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Best Local Similarity 47.55
Matches 160; Conservative
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; ORGANISM: Homo sapiens
US-11-121-086-3
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US-11±121-086-3
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US-11-121-086-16
Sequence 16, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
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Best Local Similarity 43.2%;
Matches 185; Conservative
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US-11-121-086-2
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Publication No. US20050266459A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENT
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Pred. No. 0.98;
0; Mismatches 110; Indels
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Pred. No. 5.7;
0; Mismatches 175; Indels
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CURRENT APPLICATION NUMBER: US/10/821,234
                                      PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 10
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Best Local Similarity 47.0%;
Matches 156; Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 175416
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US-10-821-234-10
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                                                     61122 GCAGGTCAGAAAATGCCACGCGTGCGCACAGAGGATGGAAGGCCAGGACCCGCCGAAG 61181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 TGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTCAAGA
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                                                                                                                                                                            61213
                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/11121086
| Publication No. US20050266459A1
| GENERAL INFORMATION: TO SERVICE ACID PROBES AND TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLE FILE FEFRENCE: 09138.6000-00000
| CURRENT APPLICATION NUMBER: US/11/121,086
| CURRENT APPLICATION NUMBER: US/11/121,086
| PRIOR RILING DATE: 2005-04
| PRIOR PILING DATE: 2005-05-04
| NUMBER OF SEQ ID NOS: 107
| SOFTWARE: PATENTIN VERSION 3.3
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.2; DE
Pred. No. 9.5;
                                                                                                                                                                      61182 CAGGGCTGTCGGGACTGGTCGCCTCTGG
                                                                                                                       973 GCTGCTGTCCAGCATCAGGTCTCCTCCCTTGG
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1171 GCTGGTGCAGCTGCTGCTGCAGCGCTGGCAGGACCCGGAGTCAGGCCTGGACTCAGCCAG 1112
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Best Local Similarity 60.4%; Pred. No. 5.5;
Matches 61; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat peptide
LOCATION: (235)...(1101)
OTHER INFORMATION: mature IGFBP-2
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                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/11090351
Publication No. US20050261230A1
GENERAL INFORMATION:
APPLICANT: Werther, George Arthur
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Guillemette, Tracy L.
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LOCATION: (1433)...(1433)
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LOCATION: (118)...(234)
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                                                                                                                                                  222 TGTGG 226
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 AGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGAGGAAGAAATCCAAGAA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 GCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGGAACCACCACGAGGAAGA 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 CCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAGGACACGAGTTGCCTAGC
APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR PRILOR DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3
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APPLICANT: DeNISE, Sue K.
APPLICANT: RERR, RICHARD
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTH, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 39; DB 7; Length 189
Best Local Similarity 46.2%; Pred. No. 11;
Matches 129; Conservative 0; Mismatches 150; Indels
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
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ORGANISM: Bovine 19866881674802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-11-121-086-16
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LENGTH: 189539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 GCCTGAGGAGACCGACTGGGTGCGATTGCCCAGCAAATGCGAAGTGTGCAAGTATGTTGC
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INFORMATION: Insulin-like growth factor binding protein
INFORMATION: (IGFBP-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wraight, Christopher John
APPLICANT: Edmondson, Stephanie Ruth
TITLE OF INVENTION: METHOD FOR THE PROPHYLAXIS AND/OR
TITLE OF INVENTION: TREATMENT OF MEDICAL DISORDERS
FILE REFERENCE: AP32556 071838.0125
CURRENT APPLICATION NUMBER: US/11/090,351
CURRENT FILING DATE: 2005-324
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 20
SOPTWARE: PSECIEC for Windows Version 3.0
SEQ ID NO 1
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NAME/KEY: allele
LOCATION: (925859)
OTHER INFORMATION: the 'n' at position 925859 may be 'c' or 'g'
                                                                                                                                                                                                                                            ION: (825765)
INFORMATION: a "c" may be deleted at this position
                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: (825828)
OTHER INFORMATION: the 'n' at position 825828 may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 'n' at position 843055 may be
INFORMATION: the 'n' at position 825401 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at position 826654 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at position 826826 may
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                                                                                  at position 825428 may
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OTHER INFORMATION: the 'n'
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INFORMATION: the
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OTHER INFORMATION: the
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OTHER INFORMATION: the
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LOCATION: (843055)
OTHER INFORMATION:
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LOCATION: (871168)
OTHER INFORMATION:
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DIHER INFORMATION:
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LOCATION: (843118)
OTHER INFORMATION:
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LOCATION: (872678)
OTHER INFORMATION:
                                                                                                                                  NAME/KEY: allele
LOCATION: (825473)
OTHER INFORMATION:
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OTHER INFORMATION:
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THER INFORMATION:
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LOCATION: (826863)
OTHER INFORMATION:
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OTHER INFORMATION:
                                         NAME/KEY: allele
LOCATION: (825428)
OTHER INFORMATION:
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NAME/KEY: allele
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NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
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             APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: BLUGart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: HERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-13-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PPLICATION NUMBER: US 60/361, 978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361, 988
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361, 988
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 228
SSOTID NO 3
FENTILE FABLESCE FOR WINDOWS VERSION 4.0
SSOTID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10928446A
; Sequence 1, Application US/20928416A
; Publication No. US20050277123A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION NUMBER: US/10/928,446A
; CURRENT APPLICATION NUMBER: 00/4-08-26
; PRIOR APPLICATION NUMBER: 60/359,741
; PRIOR APPLICATION NUMBER: 60/359,741
; PRIOR FILING DATE: 2002-02-6
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1
; LEWISTH: 1080000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 GCCATGGAGTCCATGTCTGAGCTCGCGCCCCGCTGCCTCTTATTTCCTTTGCTGCTGCTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.0%; Score 36.6; DB 7; Length 6691; Best Local Similarity 58.9%; Pred. No. 13; Matches 63; Conservative 0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CTTCCGCTGCTCCTCCTCCTGCCCCGAAGCTAGGCCCGAGTCCCGC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 chechechechecececechen 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 'n' at position 825270 may be 'c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at position 825234 may be 'c'
Kamatkar, Shubhangi
Schlegel, Robert
Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
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LOCATION: (82)...(3717)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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OTHER INFORMATION:
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LOCATION: (825270)
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: (825401)
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236760 AGTAGCTGGGATTACAGGCACCACCACCATGCCTGGCTAATTTTTTGTATTTTTAGTAG 236701
                              1547 CTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCCTTTGTCCCCCA 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
TITLE OF INVENTION: VIRAL BUDDING
FITLE OF INVENTION: VIRAL BUDDING
FILLE REFERENCE: 0.274-5795.185
CURRENT APPLICATION NUMBER: US/10/928,446A
PRIOR APPLICATION NUMBER: 60/359,741
PRIOR APPLICATION NUMBER: 60/359,741
PRIOR PILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 181
LENGTH: 1080000
                                                                                                      1607 ATCCCAGGGGCTGGAAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAG
                                                                                                                                                                                                                                                           236700 AGACTGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTTAG 236650
                                                                                                                                                                                                            FEATURE:
NAME/KEY: allele
LOCATION: (827008)..(827008)
OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: full exon 1 range is 826667-827008
                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-928 446A-181/c
Sequence 181, Application US/10928446A
Publication No. US20050277123A1
GENERAL INFORMATION:
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LOCATION: (1002118)..(1002284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (826985)..(827008)
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (843242)..(843315)
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (926021)..(926059)
OTHER INFORMATION: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1000354)....
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ORGANISM: Homo sapiens
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236760 AGTAGCTGGGATTACAGGCACCACCACCATGCCTGGCTAATTTTTTGTATTTTTAGTAG 236701 236820 CTCGGCTCACTGCAACCTCCACGCTCAAGCAGTTCTCTTGCCTCAGCCTCCCA 236761 1606 1607 ATCCCAGGGGCTGGAAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAG 1666 US-10-928-446A-183/C

Sequence 183, Application US/10928446A

Publication No. US20050277123A1

Publication No. US20050277123A1

APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VIRAL BUDDING

TITLE OF INVENTION: VIRAL BUDDING

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VARIANTS OF NEDD-IA ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION NUMBER: 02/10/928, 446A

PRIOR FILING DATE: 2002-02-26

NUMBER OF SEQ ID NOS: 202

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 183

LENGTH; 1080000 1547 CIGGGICCICATCAGCCICCAGAGIGICCCCICATCGAICTITITIGCCCTTIGICCCCCA 236700 AGACTGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTTAG 236650 1667 GTGCTGGGAGCGCCCGGGGTTTGGGGTAATCACTCACTGGCTCTCAG 1717 DB 6; Length 1080000; 84; Indels FEATURE: ; OTHER INFORMATION: full exon 30 range is 1073289-1075279 US-10-928-446A-181 OTHER INFORMATION: full exon 1 range is 826667-827008 Score 36.6; DB Pred. No. 78; 0; Mismatches FEATURE:
NAME/KEY: CDS
LOCATION: (1068609) ...(1068681)
COTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1073388) NAME/KEY: CDS LOCATION: (1067768)..(1067864) OTHER INFORMATION: exon 2.0%; NAME/KEY: CDS LOCATION: (929123)..(929176) OTHER INFORMATION: exon FEATURE: NAME/KEY: CDS LOCATION: (826985)..(827017) FEATURE: LOCATION: (922549)..(922630) OTHER INFORMATION: exon (926021)..(926059) LOCATION: (843242)..(843315) OTHER INFORMATION: exon Best Local Similarity 50.9 Matches 87; Conservative OTHER INFORMATION: exon TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: CDS LOCATION: (84) FEATURE: NAME/KEY: CDS NAME/KEY: CDS Query Match LOCATION FEATURE: FEATURE: FEATURE: 셤 à ò ò

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LOCATION: (1043121)..(1043350)
OTHER INFORMATION: exon
FRATURE:
NAME/KEY: CDS
LOCATION: (1044868)..(1044989)
OTHER INFORMATION: exon
FEATURE:
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NAME/KEY: CDS
LOCATION: (999547)..(999608)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1000354)..(1000456)
OTHER INFORMATION: exon
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LOCATION: (1050296)..(1050391)
OTHER INFORMATION: exon
FEATURE:
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LOCATION: (1006117)...(1006249)
OTHER INFORMATION: exon
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LOCATION: (1007860)..(1008036)
JTHER INFORMATION: exon
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LOCATION: (1010940)..(1011014)
OTHER INFORMATION: exon
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COCATION: (1018160)..(1018291)
JTHER INFORMATION: exon
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LOCATION: (1028113)..(1028167)
JTHER INFORMATION: exon
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LOCATION: (1034316)..(1034374)
DTHER INFORMATION: exon
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LOCATION: (1018800)..(1018919)
OTHER INFORMATION: exon
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LOCATION: (1020028)..(1020225)
JTHER INFORMATION: exon
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LOCATION: (1026659)..(1026736)
OTHER INFORMATION: exon
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LOCATION: (1047519) .. (1047589)
OOTHER INFORMATION: exon
FEATURE:
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
NAME/KEY: CDS
LOCATION: (993104)..(993154)
OTHER INFORMATION: exon
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Search completed: December 30, 2005, 04:23:29 Job time : 941 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1547 CTGGGTCCTCATCAGCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCTTTGTCCCCCA 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1607 ATCCCAGGGGCTGGAAGGCCATCACCATGAGGCTTAACCTGTCAGTTACTAGGAG 1666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.0%; Score 36.6; DB 6; Length 1080000;
Best Local Similarity 50.9%; Pred. No. 78;
Matches 87; Conservative 0; Mismatches 84; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: full exon 30 range is 1073289-1075279 US-10-928-446A-183
                                                                  NAME/KEY: CDS
LOCATION: (1062648)..(1062708)
COTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1064561)..(1064620)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1067768)..(1067864)
OTHER INFORMATION: exon
FEATURE:
LOCATION: (1060368)..(1060441)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                    LOCATION: (1066207)..(1066314)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1068609)..(1068681)
OTHER INFORMATION: exon
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LOCATION: (1073289)..(1073388)
PEATURE:
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NAME/KEY: CDS
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NAME/KEY: CDS
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AR379729 Sequence BW059085 S212P6851 BD194905 86 human CQ85523 Sequence BD218541 71 human AY267461 MUS MUSCU AC107706 MUS muscu AC164172 MUS muscu

AL928963 Mouse DNA AC020877 Mus muscu BC097110 Danio rer AC134480 Rattus no

AC138308 Mus muscu CR385039 Zebrafish

AC126550 Mus muscu CR956379 Pig DNA s

Word size :

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Sequence:

Database :

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Result Š.

AC107787 Mus muscu AC153370 Mus muscu AL662809 Mouse DNA

BC004423 Homo sapi AK090425 Homo sapi AL035587 Human DNA AK124196 Homo sapi CQ715533 Sequence U80744 Homo sapien AR379729 Sequence

OM nucleic

Run on:

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Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., McEwan, P.J., Morley, K.C., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Bahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butfersield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.B., Jones, S.J., and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC013549 1882 bp mRNA linear ROD 28-SEP-2004 Mus musculus trinucleotide repeat containing 5, mRNA (cDNA clone MGC:19340 IMAGE:4222133), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences
.. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                          BV059085
BD194905
CQ855233
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AY267461
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AC164172
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HS475N16
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AR379729
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Proc. Natl. Acad. Sci.
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Director MGC Project.
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Copyright (c) 1993 - 2005
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ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGGVQKASPLPHSPPDEL
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                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 25 Row: j Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31982623. Location/Qualifiers
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                                 WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Manil: cgapba-r@mail.nih.gov
Tissue gapba-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
http://www-abgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
     20892-2590,
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Pred. No. 0;
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/strain="FVB/N"
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| 1365 AGAACTTCCAGGACAACTCGGGTGTGGCACAAGGGGCTGGACGCCAGAGCCA 1424 1389 GGCCAGAGACTGCAGAGGCACCTGACCTAACCCCCTGGAAAGCCAATCTGCAGTTC 1448 | QY 1509 TACCAGAGTAAACACCTTTTGGCCTTTCGGTTTTGGTTCCTGGGTCCTCATCAGCCTCCAG 1568 DD 1545 TACCAGAGTAAACACCTTTTGGCTTTTGGTTTCTGGTTCCTGGGTCCTCATCAGCCTCCAG 1604 | QY 1569 AGTGLCCCTCAPCGAPCTTTTTTGCCTTTTGTCCCCCAATCCCAGGGGCTGGAAGGCCAT 1628 DD 1605 AGTGLCCCTCATCGATCTTTTTTGCCTTTGTCCCCCAATCCCAGGGGTGGAAGGCCAT 1664 | Oy 1629 CACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGGCGCCCGGGGTTG 1688 | Oy 1689 GTTTGGGGTAATCACTCACTGGCTCTCAACACTGCAGCCCCTTAATACAGTT 1748 | OY 1749 CCTTCTGTTGTGGTGACTCCCACGCCCCACACACACACATATATTTCGATGCTG 1808 | Oy 1809 TTTCATAACTGTAAAAAAAAAAAAA 1839 | T 2 644 | LOCUS AF361644 DEFINITION Mus musculus putative retinoic acid-regulated protein mRNA, Complete cds. ACCESSION AF361644 | VERSION AF361644.1 GI:14028766 KGYWORDS . SOURCE Mus musculus (house mouse) | Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (baees 1 to 1909) | AUTHORS Glozak, M.A., Li, Y., Reuille, R., Kim, K.H., Vo, M.N. and Rogers, M.B. TITLE Trapping and characterization of novel retinoid response elements JOURNAL Mol. Endocrinol. 17 (1), 27-41 (2003) PUBNED 12511604 | REFERENCE 2 (bases 1 to 1909) AUTHORS Glozak,M.B., Li,Y., Reuille,R. and Rogers,M.B. TITLE Direct Submission JOURNAL Submitted (15-MAR-2001) Biology, University of South Florida, 4202 | E. Fowler Avenue, Tampa, FL 33620, USA FEATURES Location/Qualifiers source 1. 1909 /organism="Mus musculus" | | from a reral mouse (McBurney & Kogers, Dev. Blol., 89, 503)" /cell type="embryonal carcinoma" /clone_lib="24 hr retinoic acid-treated P19 cDNA (Bouillet | et al., Dev. Biol., 170, 420)" 89919 /codon_start=1 /product="putative retinoic acid-regulated protein" |

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                Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
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Published Only in Database (2005)
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Direct Submission
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Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 20, 2002 this sequence version replaced gi:20128494. All repeats were identified using RepeatMasker: Smit, A.F. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 88 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is Completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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Submitted (10-ARR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Signary Control Collymore, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Chorpel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Rander, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hame, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matchews, C., McCarthy, M., Meldrim, C., Nacol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neal, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Sewery, P., Smith, C., Schuer, S., Schupback, R., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasailiev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                         AC117716 108992 bp DNA linear HTG 20-DEC-2002
Mus musculus clone RP23-96H4, LOW-PASS SEQUENCE SAMPLING.
AC117716
                                                                 601 GGCTCCTCCAGTGGCAGCAGCAAGCAGAAGGAAGGAACTGGGGGGGCCTGGGGGGAGGATGCC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 108992)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-96H4
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HTG: HTGS PHASE0.
Mus musculus (house mouse)
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9: gap of 100 bp

9: contig of 1140 bp in length

9: gap of 100 bp

9: contig of 1152 bp in length

9: gap of 100 bp
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7: contig of 1182 bp in length
7: gap of 100 bp
8: contig of 1165 bp in length
9: gap of 100 bp
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        Query Match
        6.8%; Score 125; DB 14; Length 108992;

        Best Local Similarity 100.0%; Pred. No. 4.7e-59;
        No. 4.7e-59;

        Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        425 AGGGTATGTCGGAGACCTTTGAGACCTGCACAACCTAGTCCACAAAGGGGTCAAGGGGTG 484
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50305 AGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAGGTGG 50364
                                                                                                                                                                                                                                                               AC074220 B9855 bp DNA linear HTG 15-MAY-2002 Mus musculus strain C57BL6/J chromosome 17 clone RP23-76I16, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Goshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R. High Throughput Mouse Sequencing Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pomerantz, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUL-2000) Department of Molecular Genetics, Albert Callege of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA Bronx, On Apr 28, 2001 this sequence version replaced gi:11276104.
                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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Ioshikhes, I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 89855)
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2: gap of unknown length
4: contig of 5942 bp in length
5: contig of 5046 bp in length
6: contig of 5046 bp in length
7: gap of unknown length
7: contig of 3491 bp in length
7: contig of 4556 bp in length
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AC074220.7 GI:13876390
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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7 88996: gap of unknown length
7 89855: contig of 859 bp in length.
Location/Qualifiers
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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL6/J"
/db xref="taxon:10090"
/chromosome="17"
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                                          note="assembly_name:Contig145"
961. .7982
estimated_length=unknown
                                                                                  983. .139<u>7</u>4
note="assembly_name:Contig144"
3925. .13944
                                                                                                                                                                                 estimated length=unknown 9011. .22501 note="assembly_name:Contig142"
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/estimated_length=unknown
22522. .27077
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17080. .49496
inte="assembly_name:Contigl33"
19497. .49516
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9517. .52236
note="assembly_name:Contig132"
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note="assembly_name:Contig131"
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54291. .56271
note="assembly_name:Contig130"
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note="assembly_name:Contig143"
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estimated
8840. .31224
note="assembly_name:Contigl39"
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note="assembly_name:Contig135"
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note="assembly_name:Contig138"
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note="assembly_name:Contigl36"
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clone="RP23-76116"
sex="male"
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                                                                                                                                                                                                                                                                                 222256 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
6070 GGAGGAAGGCCGCCCGGCTCTCTCTCTCTGGCTCCGGCTGGGCCATGGAGTCCATGTC 6011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                         6010 réadcrédédédédédédédrécréntaritédridérie 5972
                                                                                                                                                                                                                                                                                                                                                                                                                              AC134482.2 GI:25007228
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                 69
                                                                                                                                                                                                                                                                                                                   LOCUS
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VERSION
KEYWORDS
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AC134482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA, ON NOV 15, 2002 this sequence version replaced gi:23334632. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tuc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                   Submitted (27-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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3.8%; Score 69; DB 14; Length 222256;
Best Local Similarity 100.0%; Pred. No. 6.1e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107900 107999; contig of 107899 bp in length 107900 107999; gap of unknown length 108000 222256; contig of 114257 bp in length.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                     3 (bases 1 to 222256)
Rat Genome Sequencing Consortium.
                           Rat Genome Sequencing Consortium.
Direct Submission
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107900. .107999
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(bases 1 to 222256)
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ACCESSION VERSION KEYWORDS

AC131887 RESULT 7

g ઠ REFERENCE AUTHORS

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narany, Danate, Watzker, M.Lee., Abramizon, S., Adama, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Agguiano, D., Anyalabochi, V., Anyagi, A., Angodaji, M., Baca, E., Baden, H., Balabochi, V., Anyagi, A., Angodaji, M., Baca, E., Baden, H., Baladrani, V., Bandranike, D., Barber, M., Barnetend, Benahmed, F., Biswalo, K., Blati, J., Blankenburg, K., Blyth, P., Brown, M., Bayari, M., Bhay, C., Burch, E., Burch, M., Calderon, B., Devando, V., Carer, K., Calderon, E., Discher, D., Chavez, D., Chen, G., Chen, R., Chen, Y., Chener, A., Devala, M., Creek, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Devala, C., Darger, M., Creek, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Devala, C., Dargen, C., Evanic, C., Rail, C., Paderich, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Devala, C., Dargen, C., Evanic, C., Rail, C., Paderich, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Devala, C., Paderich, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Devala, C., Ferrandez, S., Filley, M., Flaggi, N., Porbes, L., Foster, M., Gaver, M., Gabisi, A., Garte, R., Garte, M., Garte, M., Gabisi, A., Garte, M., Garte, M., Garte, M., Handin, S., Hundy, M., Hamilton, K., Harnandez, S., Filly, S., Kally, S., Moreod, M., Marnoul, M., Marnou
AC131887 246404 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-3M14, WORKING DRAFT SEQUENCE, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                             AC131887
AC131887.3 GI:30466855
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                           130220 AAGAAGCGC 130228
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                                                                                                                    736 AAGAAGCGC 744
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DEFINITION
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TITLE

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Direct Submission

Submitted (19-MAY-2003) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:23270097.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using ARLas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold, biddidal sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                    Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246404)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Atlas;

Consensus quality: 238268 bases at least Q40

Consensus quality: 240099 bases at least Q30

Consensus quality: 241516 bases at least Q20

Estimated insert size: 249377; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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161358. .163910
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Center clone name: CH230-3M14
2 (bases 1 to 246404)
Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
/clone="CH230-3M14"
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                                                                                           TITLE
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                                                                                                                                                          AC135655 270958 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                  ö
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                  0; Gaps
3.8%; Score 69; DB 14; Length 246404;
100.0%; Pred. No. 6.2e-27;
tive 0, Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroides, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACISSES. 2 GI:25138854
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                    Similarity 100.
69; Conservative
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            Query Match
Best Local &
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                                                                     Matches
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:24158508.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                          Thoses 1 to 270958)

Start Genome Sequencing Consortium.

Direct Submission

Submitted (20-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 270958)
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
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Direct Submission
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/db_xref="taxon:10116"
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91405. .94036
/note="wgs_contig"
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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2.7%; Score 50; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels
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2.7%; Score 50; DB 6; Length 580;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
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Patent: WO 0151513-A 1320 19-JUL-2001;
CORIXA CORPORATION (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="n includes a,
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AX209392
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Methods for prognosis and treatment of solid tumors
Patent: WO 2004097052-A 2327 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
Location/Qualifiers
1. .526
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102157. .103191
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242793. .243897
/note="wga_contig"
246116. .248554
/note="wga_contig"
248555. .248654
/estimated length=unknown
248655. .249752
/note="wga contig"
267830. .267929
/estimated_length=unknown
/estimated_length=unknown
/estimated_length=unknown
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mol_type="unassigned DNA"

db_xref="taxon:9606"
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/note="n includes a, c,
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/note="n includes a,
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Hominidae; Homo.

It (bases 1 to 904)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butkeridato, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butkerfield, Y.S., Krzywinski, M.I., Skalaka, U., Sanilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                904 bp mRNA linear PRI 07-NOV-2003
Homo sapiens trinucleotide repeat containing 5, mRNA (cDNA clone
IMAGE:3534003), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Submitted (22-734-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Nov 6, 2003 this sequence version replaced gi:18314384.
Contact: MGC help desk
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                                                                                                                                        Length 612;
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100.0%; Pred. No. 3.7e-16;
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Tissue Procurement: DCTD/DTP
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                 2.74
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Best Local Similarity 100.0
Matches 50, Conservative
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hvlkckdtsclaegwsgkkodtaalgckkskkkssrakaaggrsssskorkelgglre
tpaprrmrasrrhplshtaplmsseptqhpvlrpsslkse"
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  PAT 31-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 612)
Zhang, Q.H., Ye,M., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z. Unpublished

2 (Dases 1 to 612)
Z (Dases 1 to 612)
Z (Dases 1 to 612)
Z (Dases 1 to 612)
Ean,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z. Direct Submission
                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                            Algate, P.A. and Mannion, J. Compositions and methods for the therapy and diagnosis of ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 3.7e-16;
tive 0; Mismatches 0; Indels
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    linear
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Homo sapiens HSPC084 mRNA, partial cds.
AF161347
    DNA
                                                                                                                                                                                                                                                                                                                              Patent: WO 0157207-A 1232 09-AUG-2001;
CORIXA CORPORATION (US)
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/tissue_type="cord blood"
<1. .431
/codon_start=3
/product="HSPC084"
AX209392 580 bp DN Sequence 1232 from Patent WO0157207.

    .580
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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db_xref="G1:6841108"
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/mol_type="mRNA"
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/clone="CBDABE11"
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FLI_CDNA.
Homo sapiens (human)
Homo sapiens
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E 1 (Dases 1 CO. 1277)
S Straubberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gascia, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Malek, J.A., Sodergren, B.J., Lux, Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Schen, S.C., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butkesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: n Column: 9. Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Sequencing Center
Center code: BCM-HGSC

Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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100.0%; Pred. No. 3.8e-16;
ive 0; Mismatches 0; Indels
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone lib="NIH MGC_12"
/lab_host="DH10B"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3457829"
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Director MGC Project.
Direct Submission
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//db_xref="GeneID:10695"
//db_xref="GeneID:10695"
//db_xref="GeneVRDTSCLAEQWSGKKGPTAALGGKKSKKKSSRAKAAGGRSSSSK QRKELGGLEGDPSPEEDEGIQKASPLTHSPPDEL"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1201)

Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.

Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.

Compositions for the detection of blood cell and immunological
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100.0%; Pred. No. 3.8e-16;
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                                       /tissue_type="Lung, small cell carcinoma"
Clone lib="NHH WGC 7"
Ab bost="DH10B-R"
/note="Vector: pOTB7"
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Homo Bapieng CDNA clone IMAGE:3457829.
BC008133
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Patent: US 6607879-A 140 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
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Sequence 140 from patent US 6607879.
AR379595
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                                                                                                                                                                                                                                                                                    /product="TNRC5 protein"
/protein_id="AAH22093.3"
/db_xref="G1:38196971"
                                                                                                                                                /gene="TNRC5"
/note="synonyms: ERDA5,
/db_xref="GeneID:10695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
db_xref="taxon:9606"
clone="IMAGE:3534003"
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                                                                                                                                                                                                                                             gene="TNRC5"
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Scoring table:

Word size :

Searched:

Minimum DB Maximum DB

Database :

Perfect score:

Sequence:

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Human Novel Human

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Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine trinucleotide repeat protein (TRP) cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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/product= "TRP"
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P-PSDB; AAU02498.
WO200130798-A1
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Score

Result

The present sequence encodes for murine trinucleotide repeat protein

(TRP). The invention describes methods of producing embryonic stem (ES)

cells comprising a heteroxygous disruption in a target DNA sequence

(preferably gene T243) encoding a TRP and of producing a knockout mouse

comprising a homozygous disruption in a gene encoding TRP, where the

comprising a homozygous disruption in a gene encoding TRP, where the

comprision of inhibits the production of the wild type TRP. The invention

also relates to identifying agents capable of affecting a phenotype of a

knockout mouse. Also described are methods of determining whether

comprision of the trinucleotide repeat in a gene encoding TRP produces a

phenotypic change. The transgenic animals and the cells are useful for

identifying compounds capable of ameliorating disease symptoms, and as

comprision of the trinucleotide repeat of section in treating

therapies and interventions which may be effective in treating

conclusions. The animal models for trinucleotide repeat disorders encourance

conclusions to study the progression of disease in vivo, the molecular

model systems to study the progression of disease in vivo, the molecular

conclusions which man and show the features observed in human disease.

Consease The animal models for trinucleotide repeat disorders are ideal

model systems to study the progression of disease in vivo, the molecular

conclusions which man and the features observed in human disease. ig the mice, it is possible to model both the p trinucleotide repeat instability in the mouse the

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424 A; 522 C; 535 G; 358 T; 0 U; 0 Other; Sequence 1839 BP;

420 480 480 540 240 240 540 9 600 99 99 720 720 120 120 180 180 300 300 360 360 420 9 TCCATGTCTGAGCTCGCGCCCCCCTTTATTTCCTTTGCTGCTGCTGCTTCCGCTG GACACGAGTTGCCTAGCAGAGCGCTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGA GGCACGAGGGAAGCGCCGCCGGGTCCGCTCTGCTCTGGGTCCGGCTGGGCCATGGAG GGCACGAGGGAGGGAGCGCCGCGCTCCCGCTCTGGGTCCGGCTGGGCATGGAG CTGCTCCTTCCTGCCCCGAAGCTAGGCCCGAGTCCCGCGGGGCTGAGGAGACCGACTGG CTGCTCCTTCCTGCCCCCGAAGCTAGGCCCGAGTCCCGCCGGGGCTGAGGAGAACCTAG rgcgattgcccagcaaatgcgaagtgtgcaagtatgttgctgtggagctgaagtcgcct TITGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGG TTTGAGGAAACGGGAAAGACCAAGGAAGTGATTGACACCGGCTATGGCATCCTGGACGGG AAGGGCTCTGGAGTCAAGTACACCAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC AAGGGCTCTGGAGTCAAGTACAAGTCGGACTTACGGTTAATTGAAGTCACTGAGACC ATTTGCAAGAGGCTTCTGGACTACAGCCTGCACAAGGAGAGGACTGGCAGCAACCGGTTT ATTTGCAAGAGCTTCTGGACTACAGCCTGCACAAGGAGGAGGACTGGCAGCAACCGGTTT GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAGGGGTCAAG GCCAAGGGTATGTCGGAGACCTTTGAGACGCTGCACAACCTAGTCCACAAAAGGGGTCAAG GTGGTGATGGATATCCCCTATGAGCTGTGGAACGAGACCTCAGCAGAGGTGGCTGACCTC Greendandeanarcecerandaderereredadadeacereadeadadeadeacere AAGAAGCAGTGTGACGTGCTGGTGGAAGAGTTTGAAGAGGTGATTGAGGACTGGTACAGG AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGTGCCAACCACGTGCTGAAGGGAAAG GACACGAGTTGCCTAGCAGAGCGGTGGTCTGGCAAGAAGGGGGACATAGCCTCCCTGGGA Gaps ô DB 4; Length 1839; Indels . 0 100.0%; Score 1839; 100.0%; Pred. No. 0; iive 0; Mismatches Query Match Best Local Similarity 100. Matches 1839; Conservative 5 61 121 121 181 181 241 241 301 301 361 361 421 481 541 541 601 601 661 661 61 421 481

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| 721 | GGGAAGAAATCCAAGAAGAGGGGGGGGGGGGTCATCCTCCCAGTGGCAGCAGCAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGA |
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| 781 | CAGAGGAAGGAACTGGGGGGCCTGGGGGGAGGATGCCAACGCCGAGGAGGAGGAGGAGGTGTG 840 |
| 841 | CAGAAGGCATCGCCCTCCCACACAGCCCCCTGATGAGCTGTGAGCCCCAGCTTAGTGTC 900 |
| 901 | CTTGAATCAAGACCCCTGACTTCAGAGCTTGGGACACGCACAGGGCAGGGCAGCT 960 |
| 961 | CCAGCAAGGACAGCTGCTGCAGCATCAGGTCTCCTCCCTTGGCTGTGCCCCTTTCCTT 1020 |
| 1021 | CCCTTGAACAACGAAGAGGAGGAACGGGTGCTGGGGAGGCGGCCCCAAAGG 1080 |
| 1081 | GAAGAGGAGGAGAGAGAGCTCTCTTTCTACACAGTCCCCCTCACGAGCTCCGG 1140 |
| | GGTCCACCAGCATCCCCAGGCTGAGATCCAGGCTCCTGACATCGAAGCTGAAGAGCATG 1200 |
| 1201 | AGGCACATAAGATGCTCACCAGGCCCCCTTCAGCCAGGAAGACTCCGTGCAGCCTCAG 1260 |
| 1261 | CAGCCAGGCCTGCTCTTCCTTCCACCAAGCATTCTCTTCTGCTGCTGGTCCTTGTCCGATGG 1320 [|
| 1321 | TAAATTCGAGAACTTCCAGGACAAACTCGGGTGTGGCACAAAGGGGCTGGACGCCAGAGC 1380 |
| 1381 1381 | CAGAGCCACGCCAGAGACTGCAGAGGGCACCTGACCTAACCCCCCTGGAAAGCCAATC 1440 |
| 1441 | TGCAGTICCCGTGTCCACCCACCCTCCTGAGGACGCCTCATGCTCTGCCCAGCCCTTCT 1500 |
| 1501 | CCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTTGGTTTGGTTCCTGGGTCCTCATCA 1560 |
| 1561 | GCCTCCAGAGTGTCCCCTCATCGATCTTTTTGCCTTTGTCCCCCAATCCCAGGGGCTGG 1620 |
| 1621 1621 | AAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGAAGCGC 1680 |
| 1681 | CGGGGTTGGTTTGGGGTAATCACTCACTGGCTCTCAGCCTTCTAACACTGCAGCCCCTTA 1740 |
| 1741 | 741 ATACAGTTCCTTCTGTTGTGGTGACTCCCACGCCCCCACACACA |

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Mismatches

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Matches 1658;

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The present sequence represents the DNA sequence of an expanded T243

gene. The T243 gene encodes for a trinucleotide repeat protein (TRP). The
invention describes methods of producing embryonic stem (ES) cells

comprising a heterozygous disruption in a target DNA sequence (preferably
gene T243) encoding a TRP and of producing a knockout mouse comprising a
homozygous disruption in a gene encoding TRP, where the disruption
inhibits the production of the wild type TRP. The invention also relates
to identifying agents capable of affecting a phenotype of a knockout
mouse. Also described are methods of determining whether expansion of the
trinucleotide repeat in a gene encoding TRP produces a phenotypic canage.
The transgenic animals and the cells are useful for identifying compounds
capable of ameliorating disease symptoms, and as test substrates for the
identification of drugs, pharmaceuticals, therapies and interventions
which may be effective in treating trinucleotide repeat disorders e.g.
fragile X syndrome and Huntington's disease. The animal models for
trinucleotide repeat disorders are ideal model system to study the
progression of disease in vivo, the molecular basis of these diseases and
show the features observed in human disease. Using the mice, it is
possible to model both the patchogenic mechanism and the trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                        ES;
                                                                                                                                                                                                                                                                     Trinucleotide repeat protein; TRP; T243; embryonic stem cell; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1848 BP; 415 A; 519 C; 543 G; 371 T; 0 U; 0 Other;
 Allen KD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Expanded TRP
                                                                                                                                                                                                                                    DNA sequence of an expanded T243 gene.
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Query Match 83.1
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Novel gene encoding protein involved in fibroblast growth factor signal transduction, useful for analyzing mechanism of formation of organs such as midbrain optic-tectum portion, cerebellum, inner ear and canceration mechanism of cell.
                                                                                                                                                      The present sequence encodes a protein involved in fibroblast growth factor (FGF) signal transduction. Such proteins are useful for analyzing the mechanism of formation of various organs, such as midbrain optictectum portion by a midbrain mesencephalon border, the mechanism of formation of cerebellum. mechanisms of formation of inner ear, blood vessils limb buds reeth, and canceration mechanisms of a cell.
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Novel transgenic animals useful as animal model for characterization function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.

Disclosure, Fig 15, 106pp, English.

ĝ Allen

Moore M,

Matthews W,

Klein R,

WPI; 2001-300473/31.

(DELT-) DELTAGEN INC

26-OCT-2000; 2000WO-US029382

WO200130798-A1

03-MAY-2001

99US-0161488P

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                                                                                                                                                                                GACAGCTGCTGTCCAGCATCAGGTCTCCTCCCTTGGCT
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The present sequence representing the DNA sequence of a deleted gene fragment of the target T243 gene is generated by using a construct comprising T243 homologous sequences (AASO5284-AASO5285). The T243 gene encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a hererozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP can of producing a knockout mouse comprising a homozygous disruption in a gene croading TRP. Where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene cacding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating calsease symptoms, and as test substrates for the identification of drugs, tharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and the trinucleotide repeat disorders e.g. fragile X syndrome and disorders are ideal model systems to study the progression of disease in civivo, the molecular basis of these diseases and show the features content mouse and the trinucleotide repeat instability in the mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 107; DB 4; Length 107; 100.0%; Pred. No. 4.5e-28; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 BP; 9 A; 42 C; 31 G; 25 T; 0 U; 0 Other;
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ES;

cell;

Trinucleotide repeat protein; TRP; T243; embryonic stem cell transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.

Mus sp. Synthetic.

DNA sequence of deleted gene fragment of target T243 gene.

(first entry)

07-SEP-2001

AAS05289 standard; DNA; 107

AAS05289

RESULT

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This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular by associating nucleic acid sequences of unknown function with particular cunknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete subcopulation where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (HSCs), as well as the nonself renewing multipotent progenitors (CMPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine HSC sub population of cells of the invention.
                                                                                                                                                                                      Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 CACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGCTGTGGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 BP; 28 A; 23 C; 31 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 GAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTG
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Pred. No. 1.4e-25;
); Mismatches 0;
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                                                                                                                                                                                                                                                          Claim 7; SEQ ID NO 4789; 123pp; English.
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100.0%; Prec
                                              (STOW-) STOWERS INST MEDICAL RES.
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03-MAY-2002; 2002US-0377383P.
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                                                                                                                                         WPI; 2004-022656/02.
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Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for predicting gene potential by subsociating nucleic acid sequences of unknown function with particular sub-population profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-population where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (HSCs), as well as the nonself renewing multipotent progenitors (CMPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine
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                                                                                                                                                                                                                                                                                                                                                             Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
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1.4e-25;
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                                                                                                                                                                                                                 (STOW-) STOWERS INST MEDICAL RES.
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Best Loca Matches

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RESULT 6 ADL88396

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Gaps

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Length 100; Indels 9

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WPI; 1995-206931/27.
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셤
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                                                                                The present sequence for T243 homologous sequence #1 is generated by PCR and is homologous to the T243 gene which encodes for a trinucleotide corpeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heteroxygous disruption in a crayet DNA sequence (preferably gene T243) encoding TRP and of producing a knockout mouse comprising a homozygous disruption in a gene cancoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotype change. The transgenic animals and the cancoding TRP produces a phenotype change. The transgenic animals and the caclls are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat cdisorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features conserved in human disease. Using the mice, it is possible to model both mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 GGAGGAAGCGCCGCCGCGCTCTCTCTGGGTCCGGCTGGGCCATGGAGTCCATGTC 68
          Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred. No. 1.1e-13;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 471 BP; 105 A; 129 C; 148 G; 88 T; 0 U; 1 Other;
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                                                               Claim 11; Fig 14; 106pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATS/) (OKUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is clamed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular fissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell
                                                                                                                                                                                                                         double
Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp.mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method, useful for prognosing and treating solid tumor, comprises comparing an expression profile of a gene expressed in peripheral blood mononuclear cells to a reference expression profile of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a method comprising comparing an expression
                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Twine NC, Slonim DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; expression profile; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; gene therapy; expression profile; solid tum
peripheral blood mononuclear cell; PBMC; prognosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function or for recognising different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.7%; Score 50; DB 2; Li
100.0%; Pred. No. 6.2e-08;
tive 0; Mismatches 0;
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                                                                                                                                                 Claim 1; Page 1501; 2245pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADU11888 standard; DNA; 526 BP
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23-JAN-2004; 2004US-0538246P.
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Immerman F, Dorner AJ;
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Best Local Similarity 100.0
---has 50; Conservative
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unaupervised clustering analysis of gene expression profiles in PBMCs of a population of patients who have the solid tumour, and where the adjustive class of patients has a first clinical outcome, and che first class of patients has a first clinical outcome, and the majority of the second class of patients has a first clinical outcome, and the majority of the second class of patients has a second clinical outcome, and cutcome. Also described are: a system comprising (i) a memory or a coutcome in a peripheral blood sample of a patient who has a solid tumour, (ii) at least one reference expression profile of the gene, (iii) a program capable of comparing the expression profile of the gene, (iii) a program, where expression levels of the gene, (iii) a program, where expression levels of the gene in peripheral blood monounclear cells of patients who have the solid tumour correlate with clinical outcomes of the patients and a nucleic acid or protein array componitiang concentrated probes for solid tumour prognosis genes is differentially expressed in PBMCs of a first class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients as compared to PBMCs of a second class of patients has a second class of patients as colid tumour prognosis gene colid tumour prognosis
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profile of at least one gene in a peripheral blood sample of a patient to at least one reference expression profile of the at least one gene, where the patient has a solid tumour, and each of the gene is differentially expressed in peripheral blood mononuclear cells (PBMCs) of a first class of patients as compared to PBMCs of a second class of patients, where both the first and second classes of patients have the solid tumour, and each of the first and second classes is a subcluster formed by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; 88; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
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. 5.2e-08;
... 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 526 BP; 111 A; 83 C; 129 G; 57 T; 0 U; 146 Other;
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live 0; Mismatches
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50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer; probe.
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Best Local S
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                                                                                                                                              The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polymucleotides, or immunogenic portions of the proteins. The ovarian tumour polymucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
                                     New polynucleotides encoding ovarian tumor proteins, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ovarian tumor proteins, and nucleic acids encoding them, used to treat and diagnose cancers, particularly ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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immunogenic; vaccine; ss.
                                                       cancer, and as probes, primers, and markers of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 580;
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                                                                                                                                                                                                                                                                                                                                                                                                  represent human ovarian tumour protein cDNA clones
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Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 50; Conservative 0; Mismatches 0;
                                                                                                                Example 1; Page 301-302; 378pp; English.
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WPI; 2001-488879/53
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                                                                            progression.
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(INCY-) INCYTE CORP.
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                                     pharmacogenomics
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26-SEP-2002;
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Thornton MB,
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development of cancer, particularly ovarian cancer. They can also be used to diagnose the onset and progression of cancer
                                                                                                                                                                                                                                   immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; metabolic disorder;
diabetes; obseity; infection; cachexia; cancer; dyslipidaemia;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; gene; ds.
                                                               Gaps
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                                                                                                                                                                                                                           Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
                                                                                  GAGGACTGGTACAGGAACCACCAGGAAGACCTGACTGAATTCCTCTG
                          Sequence 580 BP; 155 A; 136 C; 172 G; 108 T; 0 U; 9 Other;
                                            2.7%; Score 50; DB 5; Length 580;
                                                               0; Indels
                                                      5.1e-08;
                                                 100.0%; Pred. no.
                                                                                                                                                                                                          Human NOV16e coding sequence.
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2001US-0330142P.
2001US-0341058P.
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2001US-0327917P.
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2001US-0328044P.
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2001US-0328849P.
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24-OCT-2001; 2001US-0343629P
29-OCT-2001; 2001US-0349575P.
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2001US-0346357P.
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                                                                                                                                                  ACC72109 standard; DNA; 901
                                                                                                                                                                                      (first entry)
                                                               50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381625/36.
P-PSDB; ABR58397.
                                                       Local Similarity
                                                                                                                                                                                                                                                                                                              WO2003029423-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001;
12-OCT-2001;
15-OCT-2001;
17-OCT-2001;
22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001;
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   02-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001;
                                                                                                                                                                                       07-JUL-2003
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                                                                                                    353
                                                                                                                                                                     ACC72109;
                                            Query Match
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Matches
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                                                                                                                               RESULT
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                                                                                                                                                                                                       The present invention relates to novel human NOV proteins and their coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV proteins are useful in manufacturing a medicament for treating a syndrome associated with a human disease. The NOV proteins and coding sequences may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTRAN, neurotransmission-associated protein, cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective; antiantiantismonian; anticonvulsant; dermatological; nootropic; neuroprotective; antialfammatory; antithyroid; antiarthritic; anorectic; cardiant; hypotensive; hepatotropic; gene therapy; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sprague WW;
Becha SD, Khare R;
Marquis JP, Swarnakar A;
         ö
         preventing
NOVX polypeptides and nucleic acids useful for diagnosing, preventing treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NTRAN polypeptide encoding cDNA (clone ID 7523260CB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 901 BP; 221 A; 236 C; 292 G; 152 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 50; DB 8; Le
100.0%; Pred. No. 4.7e-08;
tive 0; Mismatches 0;
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JA, Yang YG, Chawla NK, Baughn MR,
MB, Mason PM, Gietzen KJ, Ison CH,
J, Jin P, Richardson TW, Tran UK)
                                                                                                                                                        Claim 20; Page 155-156; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/product= "NTRAN"
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2002US-04087B1P.
2002US-0414221P.
2002US-0426483P.
2002US-0431566P.
2002US-04317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM72164 standard; cDNA; 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-SEP-2003; 2003WO-US027411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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(NTRAM) and encoding polymuclectides. The NTRAM polypeptides can be expressed by standard recombinant methodology. The polypeptides and polymuclectides are the polypeptides and conditions associated with the decreased expression or overexpression of NTRAM, such as autoimmune/inflammatory, cardiovascular, neurological, developmental, cell proliferative, transport, psychiatric, metabolic or endocrine disorders. These diseases may include AIDS, allergies, atopic dermatitis, arthritis, thyroiditis, obesity, Parkinson's disease, troke, epilepsy, myocardial infarction, hypertension, cancer, atherosclerosis or hepatitis. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NTRAM. The NTRAM or its nucleic acid and amino acid sequences of NTRAM. The NTRAM or its cragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the carrier polymucleotide and compounds that specifically bind toor modulate the arget polymucleotide and compounds that specifically bind toor modulate the polymore and the cormodulate or antagonism of the cormodulate or antagonism or 
                                                                        diagnosing, preventing or treating diseases or conditions associated with aberrant protein expression, e.g. cancer, hepatitis, AIDS, obesity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. The present sequence represents a specific
                                                 New human neurotransmission-associated proteins and polynucleotides for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiaethmatic; antiulcer;
                                                                                                                                                                                                                                              The invention relates to human neurotransmission-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 GAGGACTGGTACAGGAACCACGGAGGAAGACCTGACTGAATTCCTCTG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                example of a polynucleotide encoding a human NTRAN polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 934 BP; 232 A; 248 C; 283 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 2.7%; Score 50; DB 12; L
Local Similarity 100.0%; Pred. No. 4.7e-08;
les 50; Conservative 0; Mismatches 0;
                                                                                                                                                                                            Claim 5; SEQ ID NO 45; 216pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE CORP.
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P-PSDB; ADM72134
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                                                                                                                                           stroke.
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Gaps

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The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, contacting the treatment of an immunopathological condition in a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes with the level of hybridisation complexes corelates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a microarray and a plurality of detectable complexes and comparing a plurality of detectable complexes and comprising a plurality of detectable complexes and comprising a plurality of detectable complexes and comprising a plurality of decince the disquession of target polymucleotides. The microarray for monitoring the expression of target polymucleotides. The microarray can be used in the expression of target polymucleotides. The microarray can be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenicity studies, forensics or pharmacogenomics. The composition complexed in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition complexed in the printed specification of a subpopulation of a form part of conversed to the printed specification but was obtained and the elected format directly such a position of the printed per person of the printed per person of the printed pers
A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
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Pred. No. 4.5e-08;
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v 100.0%; Pred. No. *..
o; Mismatches
                                                                                                                                                                 Claim 1; SEQ ID NO 140; 50pp; English.
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nes 50; Conservative
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immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchits; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node. gene; human; immunological response; blood cell; cancer; 14-AUG-2003; 2003US-00641643 98US-00023655 Human lymph node cDNA #140. US2004077003-A1. 09-FEB-1998; Homo sapiens. 22-APR-2004.

(INCY-) INCYTE CORP.

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The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response, abundantly expressed in an immunological response and/or coding for a polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and immunopathological conditions, such as AIDS, allergies, ansemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatitis, infections and arthritis. The present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site (seqdata.uspto.gov/sequence.html?DocID=2004003).
                                                                          New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications in cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1201 BP; 293 A; 342 C; 347 G; 219 T; 0 U; 0 Other;
                                                                                                                                                                                                                           Claim 15; SEQ ID NO 140; 16pp; English.
Seilhamer JJ;
Stuart SG,
                                             WPI; 2004-387937/36.
Cocks BG,
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Gaps ö Length 1201; 0; Indels Query Match
2.7%; Score 50; DB 13; L
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 50; Conservative 0; Mismatches 0;

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Search completed: December 30, 2005, 04:41:05 Job time : 1054 secs

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CF732471 BBS 04341 BBS 04341 BBS 04341 BBS 041920 BBC 061920 BBC 0623 BB

BB498921 BF785328 BB385488

AA260027 BB558801 BM223931 CN700300 BU696150

BQ714545 BB605812

BI078951

602111557 BB385488 V852c07.r BB558801

LL2in1070 L0958D12-BY705743 K0144G10-

ALIGNMENTS

BY705743 BM224022

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K0143E06-E0433C02-

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AKO86940 1199 bp mRNA linear HTC 03-APR-2004
Mus musculus 0 day neonate lung cDNA, RIKEN füll-length enriched
library, clone:B030013B02 product:1600055D17RIK PROTEIN (PUTATIVE
RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata, Craniata, Vertebrata, Euteleostomi,
Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length to CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insert sequence.
AK086940
AK086940.
HTC; CAP trapper.
Mus musculus (house mouse)
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 Genome Re
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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AUTHORS
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The FANTOM Consortium and the RIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Late 420, 563-573 (2002)

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Radchi,J., Aizawa,K., Hara,A., Hashizume,W.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamira,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakai,C.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Direct Submission
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Please visit our web site for further details.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://genome.gsc.riken.jp/.

Iccation/Qualifiers

1. 1787

rce /organism="wus musculus"

/mol_type="mxNA"

/strain="c57BL/6J"

/db_xref="Raxnor"
/db_xref="Raxnor"
/db_xref="Raxnor"
/db_xref="Laxon:1090"
/clone="E030013D02"
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ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDMYRNHQEEDLTEFLCANHVLKGKDTSCLAERWSGKKGDI
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/db xref="GI:26352265"
/translation="MESMSELAPRCLLFPLLLLLFLLLLPAPKLGPSPAGAEETDWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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DLKKQCDVLVBEFEEVIEDWYRNHGREDLTFELCANHVLKGKDTSCLAERWSCKKGDI
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'db xref="GI:26340088"
'translation="MESMSELAPRCLLFPLLLLLPLLLLPAPKLGPSPAGAEETDWVR")
Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1832)
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Please visit our web site for further details.
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/db_xref="taxon:10090"
/clone="C330027E02"
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Location/Qualifiers
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/strain="C57BL/6J"
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1832 bp mRNA linear HTC 03-APR-2004
MUS musculus ES cells cDNA, RIKEN full-length enriched library,
clone:C330027E02 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC
ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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| 1029 CAACAGCAAGAGGATCTGGGGTGCTGGGGACGGCACCCCAAAGGGAAGAGGA 108 | 1229 | 140 144 146 150 | 1469 | AGIGICCC COLLANGA COL | 0y 1689 GTTTGGGGTAATCACTGGCTCTGACGCTCTAACACTGCAGCCCCTTAATACGTT 1748 | RESULT 3 AK031742 LOCUS MUS musculus 11 days embryo head CDNA, RIKEN tull-length enriched LIDEATY, Clone:6230400B22 product:1600025D17RIK PROTEIN (PUTATIVE RETHOUG ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full insert sequence. ACCESSION AK031742. G1:26327580 KEYWORDS HTC; CAP trapper. SOURCE ORGANISM MUS musculus (house mouse) ORGANISM Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus Eukaryota; Matazoa; Chordata; Mus. Sciurognathi; Muridae; Mus. Sciurognathi; Muridae; Mus. Sciurognathi; P. and Hayashizaki, Y. TITLE High-efficiency full-length cDNA cloning PUBMED 10349636 |
|---|------|--|---|--|---|---|
| Query Match 91.9%; Score 1690; DB 4; Length 1832; Best Local Similarity 99.9%; Pred. No. 0; Matches 1790; Conservative 0; Mismatches 2; Indels 0; Gaps Qy 9 GGAGGAGCGCCGGGTCCGCTCTGGTCTGGGTCCGGCTGGAGTCCATGTC 68 Db 29 GGAGGAAGCGCCGCGGGTCCGCTCTGTTGCTGGGTCCGGCTGGGCCATGGAGTCCATGTC 88 Qy 69 TGAGCTCGCCCCGGGTCCGCTCTTATTTCCTTTGCTGCTGCTGCTGCTCCT 128 Qy 69 TGAGCTCGCCCCGCTGCTCTTATTTCCTTTTGCTGCTGCTCCTCGTTGCTCCT 128 Db 89 TGAGCTCGCCCCGCTGCTCTTATTTCCTTTTGCTGCTGCTGCTCCT 148 | | GCTC 30 CCTC 32 CCAA 36 | 369 GAGGCTTCTGGACTACAGCCTGCAAGGAGGACTGGCAGCAGCGGTTTGCCAAGGG 428 389 GAGGCTTCTGGACTACAGCCTGCACAAGGAGGAGGACCAGCACCGGTTTGCCAAGGG 448 429 TATGTCGAAGACCTTTGAGACCTGCACAAAGGGGTCAAGGGTGTGAAGGGTGTAAGAGAGGTGTAAGTGTGAAGGGTGTAAGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGGTGTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAAGGTGCTGAT 508 | 489 GGATATCCCCTATGAGCTGTGGAACGTCGCAGCAGAGGTGGCTGACCTCAAGAAGC 548 | GAGGAAGGACTGACTGAATTCCTCTGTGCCAACCACGTGAAGGGAAAGGAAAGGGAAGGG | 729 ATCCAAGAAGAGCGCAACCGAACTCAAGGCTCCTCCAGTGGCAGCAAGGAA 788 |

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KEVIDTGYGILDGKGSGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGMS
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                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome_Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer [Genome Res. 10 (11), 1757-1771 (2000)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 1684)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Adachi, I., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hangaki, T., Hiraoka, T., Hirozane, T., Hayashida, S., Furuno, M., Hangaki, T., Hiraoka, T., Hirozane, T., Hayashida, K., Mayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kondo, S., Konno, H., Konno, H., Kondo, S., Konno, H., Kondo, S., Konno, H., Kondo, S., Konno, H., Sakai, C., Matsuyama, T., Miyazaki, A., Murata, M., Oho, M., Ohasto, N., Okazaki, Y., Saito, R., Saito, R., Sakai, C., Sakai, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, Muramatsu, M., And Hayashizaki, Y.
                                                                                                                                                                                                                                                                              new genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase II Team and
              Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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  Eukaryota; Metazoa; Chordata; Craniata;
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/mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus 0 day neonate kidney DNA, RIKEN full-length enriched
library, clone:D630047M13 product:1600055D17R1R PROTEIN (PUTATIVE
RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GNE), full
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                                                                            /note="unnamed protein product; 1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE) (SPTR|Q9DAU1, evidence: FASTY, 100%ID,
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/db_xref="taxon:10090"
/clone="D630047M13"
/tissue type="kidney"
/clone_lib="RIKEN full-length er
/dev stage="0 day neonate"
82. 912
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/trainlation="MESANSELAPRCLLFPLLLLPPLLLLPPRLGPSPAGAEETDWVR
LPSKCEVCKYVAVELKSAFEETGKTKEVIDTGYGGILDGKGSWKTKSDLRLIEVTET
LCKLLDVSLAHKERTGSNRFAKGMSFTFETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKKQCDVIVVEFFERVIEDWYRNHGEEDLTFETCANIVLKGKOTSCLAERWSGKKGDI
ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL
         /tissue_type="placenta"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_gtage="adult"
72. .902
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/db_xref="taxon:10090"
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Pred. No. 0;
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/db_xref="GI:12838153"
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/strain="C57BL/6J"
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  Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600025D17 product:1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE), full
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Encyclopedia Project of Genome Exploration Research Group in Riken
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  Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
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                                                                                                                                                                                                                                  230. 685
/note="unnamed protein product; 1600025D17RIK PROTEIN
(PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA
1600025D17 GENE) (SPTR Q9DAU1, evidence: FASTY, 100%ID,
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                                                                                                                      /organism="Mus musculus"
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/strain="C57BL/6J"
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/protein_id="BAC38599.1"
/db_xref="G1:26349919"
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ASPLPHSPPDEL"
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                         /cell_type="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library'
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                                                                                    /note="unnamed protein product; 1600025D17RIK PROTEIN (PUTATIVE RETINOIC ACID-REGULATED PROTEIN) (RIKEN CDNA 1600025D17 GENE) (SPTR|Q9DAU1, evidence: FASTY, 100%10.100%1ength, match=828)
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                                                                                                                                                                                                                                                genes
                                                                                                                                                                                                                                                                                                                           Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishli,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Warahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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URL:http://genome.gsc.riken.jp/
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/db_xref="taxon:10090"
                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Group phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Adachi, I., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninoi, P., Fukuda, S., Fukunishi, Y., Ruuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraokar, T., Horl, F., Imotani, K., Ishii, Y., Itoh, M., Isawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawi, M., Tagawa, A., Takahashi, F., Tanaka, T., Tajima, Y., Toya, T., Yamamta, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramasuu, M. and Hayashizaki, Y., Yoshida, K., Submission
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/clone lib="RIKEN full-length enriched mouse cDNA library"
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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama (Ranagawa 230-0045, Japan (E-mail:Genome-rese@gsc.riken.jp, Whl:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
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Functional annotation of a full-length mouse cDNA collection
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/Globellbe="NCI_CGAP_Mam4" // Clobellbe="NCI_CGAP_Mam4" // Clobellbe="NCI_CGAP." // Clobellbe="N
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ph.D. constraint Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov.plate: LLAM10978 row: o column: 17
High quality sequence stop: 761.
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                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla
                                                                                                                                                                                                                                                                       1 (bases 1 to 766)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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/tissue type="tumor, gross
/dev stage="5 months"
/lab_host="DH108"
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/mol_type="mRNA"
/strain="NMRI"
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     J66 bp
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id and NIH Registry designation is BGO1. Positive for GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dr primer: 5'-pGACTAGTYCCGGAGCGCCCCC(T)25-3' and cloned into the ECORV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is non-normalized (normalized primary library is non-normalized normalized by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library.
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musculus cDNA clone IMAGE:6468664
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Size selected for the >1kb fragments, average insert size 1.2 kb. Normalization to Cot 7.5 . Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."
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Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 926)
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Pred. No. 1.5e-265;
                                                                                                                              36.9%; Scor.
100.0%; Pred. No. 1...
'... 0; Mismatches
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AGENCOURT 8932400 NIH MGC_94 15', mRNA sequence.
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//db xref="taxon:10090"
/clone="IMAGE:130288696"
/tissue type="embryonic limb, maxilla and mandible"
/lab_host="DH10B (phage-resistant)"
/clone lib="mNH MGC 136"
/note="Vector: pCMV-SPORT6"
/note="Vector: pCMV
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: NDAM336 row: j column: 01
High quality sequence stop: 611.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                            CTTCCCTTGAACAACAGCAGGAAGGTCTGGGGTGCTGGGAGGAGACGCCCCAA
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/organism="Mus musculus"
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AUTHORS
TITLE
JOURNAL
COMMENT
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CB320984
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us-09-696-686-47.oligo.rst

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Mus musculus
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/lab host="neting"
/lab host="neting"
/clone_lib="NIH_MGC_94"
/note="Grgan: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 %b. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imago.llnl.gov
Plate: LLAM13996 row: i column: 17
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  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6468664"
                                                                                                                                                                                                                                                                                   High quality sequence stop: 632.
Location/Qualifiers
                                            Unpublished (1999)
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Matches 663; Conservative
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AUTHORS
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.ini.gov
Tissue Procurement: Bechara Kachar and Celine Pompeia, NIDCD.
CDNA Library Preparation: Bechara Kachar (Celine Pompeia, NIDCD cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM590 row: o column: 07
High quality sequence stop: 579.
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AGENCOURT 15614073 Organ of Corti Mus musculus cDNA clone
IMAGE:30519414 5', mRNA sequence.
1200
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1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                          601 GGTCCACCCAGCATCCCCAGGGTGAGATCCAGGCTCCTGACATGGAAGCTGAAGAGCATG
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/organism="Mus musculus"

/mol_type="mRNA"

/do_txef="txexon:10090"

/dlone="th4GE:30142422"

/dlone="Th4GE:30142422"

/dlone="Th4GE:30142422"

/dlone="th="NIH MGC 135"

/note="Vector: pCMVSport6.1; Site_1: BcoRV; Site_2: NotI;

/normalized full.length enriched inbrary from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5,

14.5; and 15.5 (size selected for the 0.5-1 % fragments)

Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size_1.6k bp.

Normalization (Cot value): 7.5 kb. Priming sequence:
5.GACTAGTTCTAGATCGCGAGCGCCCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
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      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
found distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMOOSI row, k column: 07
High quality sequence stop: 609.
Location/Qualifiers
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AGENCOURT 11288067 NIH MGC_135 Mus musculus cDNA clone
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
          Pred. No. 1.3e-258;
Mismatches 0;
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          Similarity 100.
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                                                                                                                                   EST 29-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lissue type="Lateral wall of lateral ventricle"
/cell type="Early passage neurosphere"
/cell type="Rarly passage neurosphere"
/clone lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSport6.0; A cDNA library was constructed in pCMVsport6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"
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Institution of Biotechnology
AlbaNova University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378312.
601 AGGCTGAGATCCAGGCTCTTGACATGGAAGCTGAAGAGCATGAGGCACATAAGATGCTCA 660
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                             699 bp mRNA linear EST 29-DEC-:
MNSISESS Mouse Neurosphere Normalized cDNA library Mus musculus
CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                   [ (bases 1 to 699) [ Milliams, C., Wirta, V., Lundeberg, J. and Frisen, J. Expressed sequence tags of cDNA clones from murine neurospheres Unpublished (2005) [ Contact: Williams, C.
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                            CCAGCGCCCCTTCAGCCAGGAAGGACTCCGTGCAGCCTCAGCAGCC 1265
                                           Length 699;
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99.9%; Pred. No. 2.1e-248;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cecilia.williams@biotech.kth.se
Seq primer: M13REW.
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/mol_type="mRNA"
/strain="C578L/6"
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Mus musculus
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                               ACCESSION
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ACATGGAAGCTGAAGACCATGAGGCACATAAGATGCTCACCAGCGCCCCTTCAGCCAGG
                                                               1360 AAAGGGGCTGGACGCCAGAGCCAGGCCAGGCCAGAGACTGCAGAGAGGGCACCTGACCT
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Job time : 6736 secs
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IMMEDIATE SOURCE:
LIBRARY: THPINOB01
CLONE: 030137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-023-655-140
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Sequence 151343,
Sequence 151405,
Sequence 151406,
Sequence 3999
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Sequence 23380, A
Sequence 141221,
Sequence 151342,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 140, App
                                                                                                           December 30, 2005, 04:07:46; Search time 355 Seconds (without alignments) 9208.270 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-023-655-274
US-09-048-273-234
US-09-949-016-132624
US-09-949-016-13380
US-09-949-016-15138
US-09-949-016-151343
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US-09-949-016-151343
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US-09-949-016-15158
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US-08-171-385-27
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                                                                                                                                                                                                                                                                                                                         1303057 seqs, 888780828 residues
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                                                                         - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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| Sequence 27, Appl Sequence 20, Appl Sequence 20, Appl Sequence 127, App Sequence 127, App Sequence 11, Appl Sequence 1, Appl Sequence 1, Appli Sequence 1, Appli | |
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| US-08-361-441B-27 US-08-171-385-20 US-08-361-441B-20 US-09-014-969-5 US-09-205-258-127 US-10-004-860-127 US-07-973-28-11 US-07-973-28-11 US-07-974-51-1 US-07-974-51-1 US-07-976-39-1 US-07-96-397A-1 US-08-252-517-1 US-08-252-517-1 US-09-919-408A-1 US-09-919-408A-1 PCT-US92-05401-1 PCT-US92-05401-1 PCT-US92-05401-1 US-09-949-016-14960 US-09-949-016-14960 | |
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ALIGNMENTS

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US-09-03-655-140

Sequence 140 Application US/09023655

PRETER No. 6607879

GENERAL INFORMATION.

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Studart

APPLICANT: BALDARES: 1508

CORRESPONDERE ADDRESS: 1508

CORRESPONDERE: PALO ALIFORNIA

CONTRY: CALIFORNIA

COMPITER: PLOPPY disk

COMPITER: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION NUMBER: US/09/023,655

FILING DATE:

CLASSIFICATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: 37,071

REFERENCE/DOCKE
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Query Match
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; Sequence 274, Application US/09023655
; Patent No. 6607879
; APPLICANT: Suean G. Stuart
APPLICANT: Suean G. Stuart
APPLICANT: Suean G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
; CORRESSPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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100.0%; Pred. No. 4.7e-11;
ive 0; Mismatches 0; Indels
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2.0%; Score 36; DB 3; Length 153
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: HEREWITH
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CLASSIFICATION

PRIOR APPLICATION DATA:

PILING DATE:

CLASSIFICATION:

ATTORNEY/AGRAT INFORMATION:

NAME: Zeller, Karen.

REFERENCE/DOCKET NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-00;

TELECOMMUTICATION INFORMATION:

TELEPHONE: (650) 845-0555

TELEPAX: 
                                                                                                                                                                Conservative
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LIBRARY: BRSTNOT07
CLONE: 1298861
                                                                                                                  Best Local Similarity
Matches 50; Conserv
US-09-023-655-140
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                                                                                Query Match
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US-09-482-273-23/c i Sequence 23, Application US/09482273 ; Patent No. 6534631

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; Sequence 132624, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VBYTER, J. Craig et al.
; APPLICANT: VBYTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOOD.307
; CURRENT APLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFWARE: PERSESQ for Windows Version 4.0
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Sequence 15473, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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100.0%; Pred. No. 0.00051;
tive 0; Mismatches 0;
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PATENTIN VET: 2.0
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1000.0%; Pred. No. 0.45;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-482-273-23
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ORGANISM: Human
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ORGANISM: Human
US-09-949-016-141221
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; ORGANISM: Human
US-09-949-016-151342
                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Sequence 23380, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENEUE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTWARE: PRESENCE OF Windows Version 4.0

SEQ ID NO 23380
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Sequence 141221, Application US/09949016

Sequence 141221, Application US/09949016

Sequence 141221, Application US/0949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
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1.4%; Score 25; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FILENG APPLICATION NUMBER: 6/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTES FOR FAIND NOW VERSION 4.0
SEQ ID NO 15413
LENGTH: 450395
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-23380
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SEQ ID NO 141221
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SEQ ID NO 151406
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 151405
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Sequence 151406, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELEQ for Windows Version 4.0
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                           Query Match
1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 25; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151343
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151405
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US-09-949-016-151406
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                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
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Sequence 3999, Application US/09949016
; Sequence 3999, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR PRIOR DATE: 2000-00-03
; PRIOR FILING DATE: 2000-00-03
; ROUGH FILING 
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j Sequence 15158, Application US/09949016

j Retent No. 6812339

j GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WIMBER: US/09/949,016
    CURRENT APPLICATION NUMBER: US/02/11/755
    PRIOR PRILING DATE: 2000-10-20
    PRIOR PLING DATE: 2000-10-30
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v 100.0%; Pred. No. ....
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1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 25; Conservative
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US-09-949-016-15158/c
                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151406
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ORGANISM: Human
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LENGTH: 601
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Sequence 13251, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PELLING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13251

LENGTARE: DATE: DATE
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1.4%; Score 25; DB 3; Length 11211;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 25; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                              1.4%; Score 25; DB 3; Length 9087;
100.0%; Pred. No. 0.95;
tive 0; Mismatches 0; Indels
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; NAME/KEY: misc_feature
; LCCATION: (1)...(9087)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15158
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) LOCATION: (1)...(11211)

) OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13251
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Matches 25; Conservative
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US-09-949-016-13251
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Sequence 4790, Ap
Sequence 33803, A
Sequence 1232, Ap
Sequence 1232, Ap
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/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
         version 5.1.6
- 2005 Compugen Ltd.
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US-10-444-599-33803
US-01-424-599-33803
US-09-777-564-1232
US-10-015-219-1232
US-10-105-219-1232
US-10-126-103-139
US-10-126-103-139
US-10-128-072-135
US-10-128-072-135
US-10-128-072-135
US-10-128-089-135
US-10-128-089-135
US-10-128-089-135
US-10-145-746-135
US-10-175-746-135
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US-10-142-411-135
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Gapop 60.0 , Gapext 60.0
         GenCore (c) 1993
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seg length: 200000000
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US-10-430-201-4790

Sequence 4790, Application US/10430201

Sequence 4790, US20040162679A1

Sequence 4790, US20040162679A1

GENERAL INFORMATION:

APPLICANT: Li, Linheng

TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment

TITLE OF INVENTION NUMBER: US/10/430,201

CURRENT APPLICATION NUMBER: US/10/430,201

CURRENT FILING DATE: 2003-05-05

PRIOR FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 4879.
                                                                                   TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment FILE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment FILE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment CURRENT APPLICATION NUMBER: US/10/430,201
CURRENT FILING DATE: 2003-05-05
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 48779
SOFTWARE: Patentin version 3.2
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Pred. No. 2.9e-39;
); Mismatches 0; Indels
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Sequence 4789, Application US/10430201
Publication No. US20040162679A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 100; Conservative 0;
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; ORGANISM: Mus musculus
US-10-430-201-4789
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; Bublication No. U520030008299A1
; GENERAL INFORMATION:
GENERAL TOOPMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFRENCE: 210121. MND DIAGNOSIS OF OVARIAN CANCER
FILE REFRENCE: 210121. UNMABER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
; UNMBER OF SEQ ID NOS: 1739
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1232
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                                                         Query Match 2.7%; Score 50; DB 3; Le Best Local Similarity 100.0%; Pred. No. 3.4e-14; Matches 50; Conservative 0; Mismatches 0;
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2.7%; Score 50; DB 5; Lk
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0;
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Publication No. US20040038877A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John,
APPLICANT: Anderson, David W.,
APPLICANT: Boldog, Ferenc,
APPLICANT: Burgess, Catherine,
APPLICANT: Edinger, Shlomit,
OTHER INFORMATION: n = A, T, C or G
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Taupier, Raymond, jr.,
Vernet, Corine,
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Shimkets, Richard,
Smithson, Glennda,
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Gerlach, Valerie,
Gorman, Linda,
Guo, Xiaojia,
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Reiger, Daniel,
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Kekuda, Ramesh,
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Miller,
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      ; OTHER INFORMALIUS-09-777-564-1232
                                                                                                                                                                                                                                                                                         US-10-015-219-1232
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33803, Application US/10424599;
Sequence 33803, Application WS/10424599;
Publication No. US20040031072A1
GENERAL InvokMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
FILE REFERENCE: 38-21(53223)8
FULE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 33803
LENGTH: 444
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                                                                                                                                                                                                                                             454 CACAACCTAGTCCACAAAGGGGTCAAGGTGGTGATGGATATCCCCTATGAGCTGTGGAAC 513
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: OOMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.493
CURRENT APPLICATION NUMBER: 02/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
SEQ ID NO 1212
LENGTH: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100;
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2.7%; Score 50; DB 7; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                     514 GAGACCTCAGCAGAGGTGGCTGACCTCAAGAAGCAGTGTG 553
                                                                                                                                                                                                                                                                                                                                                                                 61 cagaccrcagcagaggregcrcaccrcaagaagcagrers 100
                                                                                                                                                        Query Match 5.4%; Score 100; DB 7; L. Best Local Similarity 100.0%; Pred. No. 2.9e-39; Matches 100; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: PAT_MRT3847_130528C.1
US-10-424-599-33803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1232, Application US/09777564; Patent No. US20020022591A1; GENERAL INFORMATION:
  SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(580)
                                                                TYPE: DNA
CORGANISM: Mus musculus
US-10-430-201-4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-777-564-1232
SEQ ID NO 4790
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWA FILE PRERENCE.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWA FILE OF INVENTION: WINMER: US/10/126,103

CURRENT FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US 60/284,962

PRIOR APPLICATION NUMBER: US 60/286,645

PRIOR APPLICATION NUMBER: US 60/286,645

PRIOR FILING DATE: 2001-04-26

PRIOR FILING DATE: 2001-04-19

NUMBER: OS 2002-01-09

NUMBER: OS 284
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
TITLE OF INVENTION: PATHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 6; Lt
Pred. No. 3.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 50; DB 100.0%; Pred. No. 3.2 tive 0; Mismatches
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US-10-641-643-140
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        PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 139, Application US/10431096; Publication No. US20040086896A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 139, Application US/10126103 ; Publication No. US20030224486A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%; Sc.
100.0%; Pre
0;
                                                                                                                                                                                                                                             845-4166
                                                                                                                                                                                                                                                                                                                          LENGTH: 1201 base pairs
                                                                                                                                                                                                                                             TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO: 140:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin version 3.0
SEQ ID NO 139
LENGTH: 1378
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: THP1NOB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.7%
Best Local Similarity 100.0
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-126-103-139
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Best Local Similarity
Matches 50; Conserv
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APPLICANT: Zhong, Wei THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL FILLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL FILE REFERENCE: 21402-4624

CURRENT APPLICATION NUMBER: 06/326,483

PRIOR PELING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: 60/381,101

PRIOR APPLICATION NUMBER: 60/321,342

PRIOR APPLICATION NUMBER: 60/327,342

PRIOR PELING DATE: 2002-05-16

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/328,44

PRIOR APPLICATION NUMBER: 60/328,49

PRIOR APPLICATION NUMBER: 60/328,49

PRIOR PILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/334,738

PRIOR APPLICATION NUMBER: 60/334,738

PRIOR APPLICATION NUMBER: 60/334,738

PRIOR APPLICATION NUMBER: 60/328,49

PRIOR PILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: 60/328,49

PRIOR PILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: 60/328,49

PRIOR PILING DATE: 2002-04-23

PRIOR PILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7%; Score 50; DB 7; Length 901; 100.0%; Pred. No. 3.3e-14; trive 0; Mismatches 0; Indels
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/641,643 PILING DATE: 14-Aug-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 140, Application US/10641643
Publication No. USZO040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 69
LENGTH: 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (47)..(880)
US-10-262-839-69
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Matches 50; Conserva
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US-10-641-643-140
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PRIOR FILING DATE: 2002-04-12

PRIOR PEDICACTION NUMBER: 60/327,342

PRIOR PPLICATION NUMBER: 60/327,342

PRIOR PEDICATION NUMBER: 60/328,044

PRIOR PEDICATION NUMBER: 60/328,044

PRIOR PEDICATION NUMBER: 60/328,849

PRIOR PEDICATION NUMBER: 60/328,849

PRIOR FILING DATE: 2001-10-12

PRIOR FILING DATE: 0002-04-23

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 367

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 67

LENGTH: 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1596;
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100.0%; Pred. No. 3.1e-14;
Live 0; Mismatches 0;
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TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR FLING DATE: 1997-09-17
PRIOR FLING DATE: 1997-09-17
PRIOR FLING DATE: 1997-09-17
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Publication No. US20030004311A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/371,972
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Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DeForge, Laura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (388)..(549)
US-10-262-839-67
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PPLICANT: Zhong, Mei
TILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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2.7%; Score 50; DB 7; Length 1378;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/262,839
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PLING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
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PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
                   CURRENT APPLICATION NUMBER: US/10/431,096
CURRENT FILING BATE: 2003-05-07
PRIOR PAPLICATION NUMBER: US 60/284,962
PRIOR PILING DATE: 2001-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/286,645
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-04-26
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 307
SOFTWARE: PALENT NOS: 307
SOFTWARE: PALENT NOS: 307
LENGTH: 1378
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Publication No. US20040038877A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John,
APPLICANT: Anderson, David W.,
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Vernet, Corine,
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Burgess, Catherine,
Catterton, Elina,
Edinger, Shlomit,
Ellerman, Karen,
Gerlach, Valerie,
Gorman, Linda,
Guo, Xiaojia,
Ji, Welzhen,
Kekuda, Ramesh,
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Reiger, Daniel,
Rothenberg, Mark,
Shimkets, Richard,
Smithson, Glennda,
Spytek, Kimberly,
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Miller, Charles,
    FILE REFERENCE: D0108A CIP
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; ORGANISM: Homo sapiens
US-10-431-096-139
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US-10-262-839-67
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| NUMBER: 60/059352 1997-09-19 NUMBER: 60/05988 1997-09-19 NUMBER: 60/059836 1997-10-17 NUMBER: 60/062250 1997-10-17 NUMBER: 60/062285 1997-10-17 1997-10-17 | | 1. 1997-11-21 NUMBER: 60/06653 1. 1997-11-24 NUMBER: 60/066511 1. 1997-11-24 NUMBER: 60/069212 1. 1997-12-11 NUMBER: 60/069218 1. 1997-12-11 NUMBER: 60/069334 1. 1997-12-11 NUMBER: 60/069334 1. 1997-12-11 NUMBER: 60/06934 1. 1997-12-12 NUMBER: 60/07330 1. 1998-01-23 NUMBER: 60/07330 1. 1998-01-23 NUMBER: 60/07320 1. 1998-02-04 NUMBER: 60/073612 1. 1998-02-09 NUMBER: 60/074086 1. 1998-02-09 NUMBER: 60/074092 1. 1998-02-09 NUMBER: 60/074092 |
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PRICIN FILING DATE: 1998-03-10
PRICIN PRICIATION UNDERS: 60/07924
PRICIN PAPICATION NUMBER: 60/07924
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PRICIN PLICATION NUMBER: 60/07928
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PRICIN PLICATION NUMBER: 60/09129
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RESULT 14
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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100.0%; Pred. No. 3.1e-14;
Live 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FLING DATE: 1998-06-24
PRIOR FLING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-36
PRIOR PLING DATE: 1998-06-36
PRIOR APPLICATION NUMBER: 60/09083
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PPLING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
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Publication No. US20030017563A1
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Stewart, Timothy A
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Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Matches 50; Conservative
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Best Local Similarity 100.
Matches 50; Conservative
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ORGANISM: Homo Sapien
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US-10-121-049-135
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APPLICANT:
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Sequence 135, Application US/10121049 Publication No. US20030022239A1 GENERAL INFORMATION:

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIL17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
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100.0%; Pred. No. 3.1e-14;
iive 0; Mismatches 0;
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Publication No. US20030022328A1
GENERAL INFORMATION:
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Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Desnoyers, Luc
Filvaroff, Ellen
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                                                                        Goddard, Audrey
                                                                        Gao, Wei-Qiang
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CORGANISM: Homo Sapien
US-10-123-904-135
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US-10-121-049-135
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Best Local Similarity
Matches 50; Conserv
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED SECOPING THE SAME
PILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT PILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
LENGTH: 1675
                                        0; Gaps
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                                                                                                    Query Match 2.7%; Score 50; DB 5; Length 1675; Best Local Similarity 100.0%; Pred. No. 3.1e-14; Matches 50; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                 RESULT 15
US-10-140-470-135
Sequence 135, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                 DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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Smith, Victoria
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ORGANISM: Homo Sapien
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APPLICANT:
APPLICANT:
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Search completed: December 30, 2005, 09:34:20 Job time : 1383 secs

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December 30, 2005, 04:41:12 ; Search time 299 Seconds (without alignments) 3224.269 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                       4172979 segs, 262114271 residues
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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1839
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                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published Applications NA New:*

1: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/DS07 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US11 NEW PUB.seq:*

Database :

| SUMMARIES * | Query Score Match Length DB ID Description | 50 2.7 1675 6 US-10-131-826A-135 Sequence 135, App | 1.4 25 7 US-11-121-849-665859 | 1.4 25 7 US-11-121-849-665860 | 6 US-10-750-185-35528 | 1,4 1833 6 US-10-750-185-38459 | | 24 1.3 25 7 US-11-121-849-665854 Sequence 665854, | 24 1.3 149111 7 US-11-112-908-63 Sequence 63, Appl | 154548 7 US-11-121-086-33 Sequence 33, | 64, | 1-121-086-30 Sequence 30, | 62, | 36, | 65, | 32, | 65857 | 23 1.3 946 6 US-10-750-185-37066 Sequence 37066, A | | 23 1.3 1382 6 US-10-750-185-39793 Sequence 39793, A | 1,3 1445 6 US-10-750-185-29927 Sequence | 1,3 2352 6 US-10-909-125-835 | 3 1.3 10166 7 US-11-147-606-3 Seguence 3, A | |
|----------------|---|--|-------------------------------|-------------------------------|-----------------------|--------------------------------|------|---|--|--|--------|---------------------------|------|------|------|------|-------|--|------|---|---|------------------------------|---|--|
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| | Sequence 8, Appli | Sequence 18671, A | Seguence 35450, A | Sequence 35535, A | Sequence 43529, A | Sequence 46985, A | Sequence 47049, A | Sequence 50304, A | Sequence 50700, A | Sequence 50702, A | Sequence 50871, A | Sequence 53197, A | Sequence 58387, A | Sequence 80946, A | Sequence 82910, A | Sequence 2, Appli | | Sequence 21696, A | Sequence 54079, A | Sequence 24, Appl | Sequence 38, Appl |
|------------------|-------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|---------------------|-------------------|-------------------|
| US-11-112-908-23 | US-11-121-086-8 | US-10-995-561-18671 | US-10-995-561-35450 | US-10-995-561-35535 | US-10-995-561-43529 | US-10-995-561-46985 | US-10-995-561-47049 | US-10-995-561-50304 | US-10-995-561-50700 | US-10-995-561-50702 | US-10-995-561-50871 | US-10-995-561-53197 | US-10-995-561-58387 | US-10-995-561-80946 | US-10-995-561-82910 | US-11-156-909-2 | US-10-750-185-27071 | US-10-750-185-21696 | US-10-750-185-54079 | US-11-156-909-24 | US-10-986-501-38 |
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| 23 | 23 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 |
| 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
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ALIGNMENTS

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Sequence 115.4 Application US/10131826A
PUBLICANT BARET, Kevin P.
APPLICANT BARET, Kevin P.
APPLICANT BARET, Kevin P.
APPLICANT BETESTIA, Wauteen
APPLICANT BETESTIA, Wauteen
APPLICANT BETESTIA, Wauteen
APPLICANT Godwell, Paul J.
APPLICANT Godwell, Paul J.
APPLICANT Godwell, Paul J.
APPLICANT GOGwell, Paul J.
APPLICANT GOGWEL, Paul J.
APPLICANT HARS, DEAL AND TRANSNERRANE POLYPEPTIDES AND NUCLEIC TILLE BEFRERENE ED SID TRANSNERRANE FOLICATION NUMBER GO/05911
PRIOR APPLICATION NUMBER GO/05914
PRIOR APPLICATION NUMBER GO/05915
PRIOR PLING DATE: 1997-06-17
PRIOR APPLICATION NUMBER GO/05915
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER GO/05916
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER GO/05916
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Gaps
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                                                                                                                                                                  Sequence 35528, Application US/10750185

Publication No. US200266603A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSNEELD, David
APPLICANT: ROSNEELD, David
APPLICANT: BATES, Stephen
APPLICANT: PATTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARR: PATENCE NOS: 64922
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APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILINO-2
CURRENT APPLICATION NUMBER: US 60/437,482
FRIOR PILING DATE: 2002-12-31
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VETRION 3.1
SEQ ID NO 38459
LENGTH: 1833
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Pred. No. 0.56;
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Pred. No. 0.55;
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1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 25; Conservative 0; Mismatches
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1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 25; Conservative 0; Mismatches
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; Sequence 38459, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1815 AACTGTAAAAAAAAAAAAAAAAA 1839
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                   606 CCAGGAGGAAGACCTGACTGAATTC 630
                                                              1 ccaggaggaagaccrgacrgaarrc 25
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US-10-750-185-35528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bovine 19866880774774
US-10-750-185-38459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
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Sequence 665860, Application US/11121849

Sequence 665860, Application US/11121849

Publication No. US20050272080A1

GENERAL INPORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT FILING DATE: 2005-05-03

CURRENT FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 665859, Application US/11121849

Sequence 665859, Application US/11121849

GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded FILE REFERENCE: 3684.1

FILE REFERENCE: 3684.1

CURRENT APPLICATION UNMER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR APPLICATION NUMBER: 60/567,949
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 135
LENGTH: 1675
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100.0%; Pred. No. 8.3e-11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 665859
LENGTH: 25
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                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 50; Conservative
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nes 25; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-665860
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CORGANISM: Homo sapien
US-11-121-849-665859
                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapien
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US-11-121-849-665859
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Best Local Si
Matches 25;
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Sequence 33, Application US/11121086
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE REPERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILLIG DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 2005-05-04
PRIOR PILING DATE: 2004-05-04
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Pred. No. 0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 24; DB 7;
100.0%; Pred. No. 0.64;
tive 0; Mismatches
APPLICANT: Davis, Lisa M.
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REPERBRES: 04-164-04-164-05
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR PLIING DATE: 2004-06-01
PRIOR PLIING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PLIING DATE: 2004-11-30
PRIOR PLIING DATE: 2004-11-30
PRIOR PLIING DATE: 2004-11-30
PRIOR PLIING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 24; Conservative 0; Mismatches
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136117 ACTGTAAAAAAAAAAAAAAAAAAAA 136094
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CURRENT FILING DATE: 2005-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1816 ACTGTAAAAAAAAAAAAAA 1839
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PRIOR APPLICATION NUMBER: US 60/564,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/11112908; Publication No. US20050260659A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
....hag 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-11-112-908-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          149111
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LENGTH: 154548
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US-11-112-908-64/c
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Sequence 665854, Application US/11121849

Sequence 665854, Application US/11121849

Sequence 665854, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT PILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-06-03

NUMBER OF SEQ ID NOS: 673904

SOUTHWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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                                                                             Sequence 55, Application US/11112908
Publication No. US2005026065941
GENERAL INCRMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Beast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR PILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
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; Sequence 63, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-112-908-55
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; ORGANISM: Homo sapien
US-11-121-849-665854
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Matches 25
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NUMBER OF SEQ ID NOS: 511
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APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR FILING DATE: 2005-05-04
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1.3%; Score 24; DB 7; Length 157230;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 24; Conservative 0; Mismatches 0; Indels 0
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Publication No. US2005060659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
CURRENT APPLICATION NUMBER: US 60/54,758
PRIOR PELICATION NUMBER: US 60/54,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-01-30
PRIOR PILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR PILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin version 3.3
SEQ ID NO 64-3
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SOFTWARE: Patentin version 3.3
SEQ ID NO 50
LENGTH: 158692
                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-64
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ORGANISM: Homo sapiens
US-11-121-086-30
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US-11-121-086-30
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APPLICANT: DOULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 00/567,570
PRIOR APPLICATION NUMBER: 00/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 36
LENGTH: 172649
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Pred. No. 0.62;
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE OF INVENTION: Breast Cancer Biomarkers
FILE OF INVENTION: US 6011/112,908
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-10-10
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR PRILING DATE: 2004-11-30
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; Publication No. US20050266459A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3 SEQ ID NO 62 LENGTH: 170508
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SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                               Best Local Similarity 100.
Matches 24; Conservative
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CORGANISM: Homo sapiens
US-11-112-908-65
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US-11-121-086-36
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US-11-112-908-62
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LENGTH: 173115
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Query Match 1.3%; Score 24; DB 7; Length 173115; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 24; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                   RESULT 15
US-11-112-908-32
Sequence 32, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Breast Cancer Biomarkers
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2006-04-22
PRIOR APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-01-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PALCHTON NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
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Search completed: December 30, 2005, 09:39:32 Job time : 302 secs 84066 ACTGTAAAAAAAAAAAAAAA 84089 원

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